

GenCore version 5.1.6
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M nucleic - protein search, using frame_plus_n2p model

un on: March 9, 2004, 08:52:43 ; Search time 153 Seconds
(without alignments)
12805.127 Million cell updates/sec

itle: US-09-719-272-1

erfect score: 1138

equenece: 1 gatccggactgaagactccc.....atttgataatcagatttct 3467

coring table:

OLIGO 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

earched: 1586107 seqs, 282547505 residues

ord size: 1

total number of hits satisfying chosen parameters: 2987630

minimum DB seq length: 0

maximum DB seq length: 2000000000

ost-processing: Listing first 45 summaries

ommand line parameters:

MODEL=frame+ n2p.model -DEV=xlp
Q/cgn2_1/USPTO.spool_p/US09719272/runat_09032004_085229_7428/app_query.fasta_1.3655
DB=A Geneseq 29Jan04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
LIST=45 -DOCLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
USR=US09719272 -CGN_1_121 -runat_09032004_085229_7428 -NCPU=6 -ICPU=3
NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFLOCCK=100 -LONGLOG
DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

atabase : A Geneseq 29Jan04.*

1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	607	53.3	607	3	RAY81783 Human pro
2	607	53.3	607	3	RAY56098 LAR tyros
3	607	53.3	647	4	RAM23746 Human EST
4	607	53.3	647	4	RAU14379 Human nov
5	607	53.3	1796	6	AAE37971 Human kin
6	607	53.3	1897	3	AAE37971 Human pro
7	607	53.3	1897	3	AAE37971 Human pro
8	607	53.3	1897	3	AAE37971 Human pro
9	607	53.3	1897	7	ADD18740 Human dis
10	607	53.3	1907	4	AAU14143 Human nov

11	442	38.8	442	3	AA556372	AA556372 Human pro
12	296	26.0	296	7	ABW78984	ABW78984 Human leu
13	202	17.8	306	4	AA578268	AA578268 Human DCA
14	197	17.3	294	4	AA578287	AA578287 Human BCA
15	141	12.4	250	4	AA593370	AA593370 Human pro
16	136	12.0	245	4	AA593389	AA593389 Human pro
17	59	5.2	1501	2	AA572858	AA572858 Rat recep
18	59	5.2	1863	7	ADD46989	ADD46989 Rat Prote
19	59	5.2	1904	5	ABBS7100	ABBS7100 Mouse isc
20	59	5.2	1911	2	AA571726	AA571726 Human pro
21	59	5.2	1911	2	AAW27225	AAW27225 Human pro
22	59	5.2	1911	2	AAW94027	AAW94027 Human pro
23	59	5.2	1911	4	AAU01459	AAU01459 Human pro
24	59	5.2	1948	7	ADD18742	ADD18742 Human dis
25	59	5.2	1949	7	ADE57117	ADE57117 Human pro
26	59	5.2	1949	7	ADE57121	ADE57121 Human pro
27	59	5.2	1949	7	ADD47019	ADD47019 Human pro
28	59	5.2	1949	7	ADD47015	ADD47015 Human pro
29	54	4.7	1291	2	AA575201	AA575201 Tyrosine
30	44	3.9	154	2	AA56458	AA56458 Murine pr
31	40	3.5	1496	5	ABBS7380	ABBS7380 Rat mucoc
32	40	3.5	1496	7	ADE57115	ADE57115 Rat Prote
33	40	3.5	1496	7	ADE57119	ADE57119 Rat Prote
34	40	3.5	1496	7	ADD47013	ADD47013 Rat Prote
35	40	3.5	1496	7	ADD47017	ADD47017 Rat Prote
36	34	3.0	2037	4	ABB71928	ABB71928 Drosophil
37	14	1.2	14	2	AA57006	AA57006 LAR prote
38	14	1.2	176	2	AA560876	AA560876 Product o
39	14	1.2	322	2	AA560877	AA560877 Mouse PTP
40	14	1.2	405	2	AA589251	AA589251 Mouse PTP
41	14	1.2	426	2	AA589249	AA589249 Mouse PTP
42	14	1.2	463	2	AA589250	AA589250 Mouse PTP
43	14	1.2	1959	6	AA537322	AA537322 Human rec
44	14	1.2	2281	5	AAO18736	AAO18736 Human NOV
45	14	1.2	2291	6	ABP60057	ABP60057 Human pho

ALIGNMENTS

RESULT 1

AA581783

ID AA581783 standard; protein; 607 AA.

XX

AC AA581783;

XX

DT 07-JUN-2000 (first entry)

XX

DE Human protein tyrosine phosphatase specific antibody protein sequence.

XX

KW Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR;

KW CD45; PTP; diagnosis; insulin resistance related disease; syndrome X;

KW non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;

XX heart disorder.

XX

OS Homo sapiens.

XX

FN WO200002922-A1.

XX

PD 20-JAN-2000.

XX

PF 06-JUL-1999; 99WO-JP003656.

XX

PR 10-JUL-1998; 98WO-JP003120.

XX

PA (FUSO) FUSO PHARM IND LTD.

XX

PI Yamamoto H, Tsujikawa K, Uchino Y;

XX

DR WPI; 2000-182215/16.

DR N-PSDB; AA291907.

XX

PT Antibody for diagnosis and treatment of insulin resistance disorders and

PT syndrome X recognises the intracellular domains of tyrosine kinases.

XX Claim 6; Page 53-59; 83pp; Japanese.
XX This sequence is an antibody of the invention that has sites specifically
CC recognising the intracellular domains of the phosphatase subunits LAR and
CC CD45. The antibody recognises the intracellular domain of two or more
CC protein tyrosine phosphatases (PTPs). The antibody is useful for the
CC detection and assay of ptp including novel phosphatases generated by
CC cloning; and diagnosis, treatment and prevention of insulin resistance
CC related diseases and non-insulin dependent diabetes mellitus, syndrome X
CC and arteriosclerosis and heart disorders
XX Sequence 607 AA;
SQ

Alignment Scores:
Pred. No.: 0 Length: 607
Score: 607.00 Matches: 607
Percent Similarity: 100.00% Mismatches: 0
Best-Local Similarity: 100.00% Indels: 0
Query Match: 53.34% Gaps: 0
DB: 3

US-09-719-272-1 (1-3467) x AAY81783 (1-607)

QY	6	GGACTGAAGGACTCTCTGCGCCACTCTCTGACCTGTGGAGATCGGAGGCTCAAC	65
DB	1	GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgLeuAsn	20
QY	66	TACCAGAGCCAGGATGCGAGACCAACCCACCCATCCCATCCAGCCACCTGCGGACAC	125
DB	21	TyrGlnThrProGlyMetArgAspHisProProlieThrAspLeuAlaAspAsn	40
QY	126	ATCGAGCGCTCAAGCCAGACCAAGTGGCTCAAGTCTCCAGAGATGAGTCCATCGAC	185
DB	41	IleGluArgLeuLeuAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp	60
QY	186	CCTGACAGCAGCTTCACTGCGGAGAAATCAAACTGGAGGTGAACAGCCCAAGAACCGC	245
DB	61	ProGlyGlnGlnPheThrTyrGluAsnSerAsnLeuGluValAsnLysProLysAsnArg	80
QY	246	TATGGAATGTCATCGCTACAGCACTCTGAGTCATCTTACTCTATCGATGGGCTC	305
DB	81	TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal	100
QY	306	CCCGGAGTGACTACATCAATCCCAACTACATCGATGCTACCGCAGCAGCAAGTCCCTAC	365
DB	101	ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr	120
QY	366	ATCGCCACGACGGCCCTGCGCAGACCAATGGCGATTTCTGGAGAAATGGTGGGAA	425
DB	121	IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTyrArgMetValTyrGlu	140
QY	426	CAGCGCAGCGGCTGCTGATGATGACACGCTGGAGGAGAGTCCCGGTAAATGT	485
DB	141	GlnArgThrAlaThrValValMetMetThrArgLeuGluLysSerArgValLysCys	160
QY	486	GATCAGTACTGCCACCGCTGCGCAGACCAATGGCGATTTCTGAGTACCTGCTGTG	545
DB	161	AspGlnTyrTyrProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu	180
QY	546	GACACAGTGGCTGCGCACATACATGTCGACCTTCGCACTCCCAAGAGTGGCTCC	605
DB	181	AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer	200
QY	606	AGTGAGAGCGTGGCTGCTGAGTTTCAGTTTCATGGCTGGCCAGACCATGGAGTTCCT	665
DB	201	SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTyrProAspHisGlyValPro	220
QY	666	GAGTACCCCACTCCATCTGCTGCTTCTTACACGGGTCAAGGCTGCAACCCCTGAC	725
DB	221	GluTyrProThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAsp	240
QY	726	GCAGGGCCCATGTGTGTCACCTGACGCGGGCGTGGCCGACCCGCTGCTTCATCGTG	785

DB	241	AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal	260
QY	786	ATTGATGCTATGTTGGAGCGGATGAGCAGAGAGCGGTGGACATCTATGGCCAGTG	845
DB	261	IleAspAlaMetLeuGluArgMetLysHisGlnLysThrValAspIleTyrGlyHisVal	280
QY	846	ACCTGCTCATGCTACACAGAGAACTATCATGTTGTCAGACGGAGGCCAGTGTTCATC	905
DB	281	ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle	300
QY	906	CATGAGGCGCTGCTGAGGCTGCCACGTCGGCCACACAGAGAGTGCCTGCCGCAACCTG	965
DB	301	HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu	320
QY	966	TATGCCCATCATCAGAAAGCTGGCCCAAGTCTCCAGGGGAGAGTGTACCCCATGGAG	1025
DB	321	TyrAlaHisIleGlnLysLeuGlyGlnValProGlyGluSerValThrAlaMetGlu	340
QY	1026	CTCGAGTTCAAGTTCCTGCTGCGCCAGCTCCAGGCCCAACAGTCCCGCTTCATCAGCGCCAC	1085
DB	341	LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn	360
QY	1086	CTGCCCTGCAACAAGTTCAGAAACCGGCTGGTGAACATCATGCCCTACGAATTGACCGGT	1145
DB	361	LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg	380
QY	1146	GTGTGTCTCAGCCCATCCGCTGTGTGAGGGCTCTGACTACATCATCATGCTTCCTG	1205
DB	381	ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu	400
QY	1206	GATGTTTATAGACAGCAGAAAGCCCTACATAGTACACAGGGGCTCTCGCAGAGACACC	1265
DB	401	AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr	420
QY	1266	GAGGACTTCTGGCGCATGCTATGGAGCACAATTCACCATCATGCTCATGCTGACCAAG	1325
DB	421	GluAspPheTyrArgMetLeuTyrGluHisAsnSerThrIleIleValMetLeuThrLys	440
QY	1326	CTTCGGGACATGGCAGGAGAAATGCCACAGTAGTACTGGCCAGCAGAGCGCTCTCTCGC	1385
DB	441	LeuArgGluMetGlyArgGluLysCysHisGlnTyrTyrProAlaGluArgSerAlaArg	460
QY	1386	TACCACTACTTTGTTGATCCCGATGCTGAGTACACATGCTCCCGCATATCTCGGT	1445
DB	461	TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg	480
QY	1446	GAGTTCAGGTCAAGTCAAGGATCGCGGATGGCAGTCAAGCAATCCGCGAGTTCAGTTC	1505
DB	481	GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe	500
QY	1506	ACAGACTGCGCAGCAGCGCGCTGCCAAGACAGCGGAGGGATTCTTGTCTTCATCGGG	1565
DB	501	ThrAspTyrProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly	520
QY	1566	CAGTGCATATAGCAGGAGCAGTTCGACAGGATGGCCCTATCAGCTGACATGCTCTGGAGCGCATGGC	1625
DB	521	GlnValHisLysThrLysGlnPheGlnAspGlyProIleThrValHisCysSer	540
QY	1626	GCTGGCGCTGGCGGACCGCGGTGTTTCATCTCTGAGCATGCTCTGGAGCGCATGGC	1685
DB	541	AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg	560
QY	1686	TATGAGGGGTGCTGACATGTTTCAGACCGTGAGACCCCTCGGTACACAGCGCTCTGCC	1745
DB	561	TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla	580
QY	1746	ATGGTGCAGACAGACAGCAGTATCAGTGTGTCTACCGTGGCGGCTTGGAGTACCTCGC	1805
DB	581	MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaLeuGluTyrLeuGly	600
QY	1806	AGCTTTGACCATTCGCAACG	1826

Db 441 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 460
1386 TACCAGTACTTTGTTGTTGACCCGATGGCTGAGTACAACATGCCAGTATATCTCTGCGT 1445
Db 461 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 480
1446 GAGTTCAAGTCAAGTATGCGCGGATGGCAGTCAAGGACATCCGGCAGTCCAGTTTC 1505
Db 481 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 500
1506 ACAGCTGGCCAGAGCAGGGCGTGGCCCAAGACAGCGGAGGATTCATTGACTTCATCGGG 1565
Db 501 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 520
1566 CAGTGCATAGACCAAGAGCAGTGTGGAGAGATGGGCTATCAGGTGCACTGCAGT 1625
Db 521 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 540
1626 GCTGGCGTGGCCCGCCACCGGGGTGTTTCATCTCATCTGAGCATCGTCTGGAGCGCATCGCG 1685
Db 541 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluA-gMetArg 560
1686 TATGAGGGCGTGGTGCACATGTTTCAGACCGTGAAGACCCCTGGGTACACAGCTCTGCGC 1745
Db 561 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 580
1746 ATGTTGCAGACAGAGGACCATATCAGTGTGTACCGTGGCGGCTGGAGTACCTCGGC 1805
Db 581 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 600
1806 AGCTTTGACCACTATGCAACG 1826
Db 601 SerPheAspHisTyrAlaThr 607

RESULT 3

AAAM23746

ID AAAM23746 standard; protein; 647 AA.

XX AC

XX AAAM23746;

XX 12-OCT-2001 (first entry)

XX Human EST encoded protein SEQ ID NO: 1271.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

XX diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;

XX gene therapy; nutrition.

XX Homo sapiens.

XX WO200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US002687.

XX 25-JAN-2000; 2000US-00491404.

XX 17-JUL-2000; 2000US-00617746.

XX 03-AUG-2000; 2000US-00631451.

XX 15-SEP-2000; 2000US-00663870.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

XX Cao Y, Drmanac RA, Zhang J, Werhman T;

XX WPI; 2001-476164/51.

XX N-PSDB; AAH98405.

XX Isolated polypeptide for treatment of diseases, diagnostics, raising

XX antibodies and research use.

XX

PS Claim 20; Page 916-917; 1275pp; English.
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention

XX Sequence 647 AA;

Alignment Scores:
Pred. No.: 0 Length: 647
Score: 607.00 Matches: 607
Percent Similarity: 100.00% Conservations: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.34% Indels: 0
DB: 4 Gaps: 0

US-09-719-272-1 (1-3467) x AAAM23746 (1-647)

QY 6 GGACTGAAGGACTCTTGTGCTGGCCACTCTCTGACCTGTGGAGTGGGAGGCTCAAC 65
Db 41 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgGluLeuAsn 60
QY 66 TACCAGACCCAGGATGTCGAGACACCCACCCATCCCATCCAGCTGGCGGCAAC 125
Db 61 TyrGlnThrProGlyMetArgAspHisProIleThrAspLeuAlaAspAsn 80
QY 126 ATCGAGCGCTCAAGCCCAACGATGGCTCAAGTCTCCAGGAGTATGATGCTCATGAC 185
Db 81 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 100
QY 186 CTGGACAGCAGCTTCACGTGGGAGAAATCAACCTGGAGGTGAACCAAGCCCAAGACCGC 245
Db 101 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 120
QY 246 TATCGAATGTCATCGCTACGACCATCTCTCGAGTATCTTACTCTATCATGCTGGGTC 305
Db 121 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 140
QY 306 CCGGGAGTGACTACATCAATGCCAATCATCATGCTACCGCAAGCAGAGTCCCTAC 365
Db 141 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 160
QY 366 ATCGCCACGCGGGCCCTGCTGCCAGACCATGGCGGATTTCTGAGAAATGCTGGGAA 425
Db 161 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTyrArgMetValTrpGlu 180
QY 426 CAGCCGACGGCCACTGTGTCATGATGACCGCTGGAGGAGAGTCCCGGTAAATGT 485
Db 181 GlnArgThrAlaThrValMetMetThrArgLeuGluLysSerArgValLysCys 200
QY 486 GATCAGTACTGCGCCAGCCGTCGACACCGACCTGTGCTTATTCAGGTGACCTGTG 545
Db 201 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 220
QY 546 GACACAGTGGAGCTGCCACATACACTGTGCGACCTTCGCACTCCCAAGAGTGGCTCC 605
Db 221 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 240
QY 606 AGTGAAGCGTGAGTGGCTCAGTTTCAGTTTCATGCTGCGCCAGACCATGAGTTCTCT 665
Db 241 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 260
QY 666 GAGTACCCCAACTCCCATCTGCTGCTTCTAGACGGGTCAAGGCTGCAACCCCTAGAC 725
Db 261 GluTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 280
QY 726 GCAGGGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 785

281 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 300
2y
786 ATTGATGCCATGTTGGAGCGGATGAGACGAGACGCGTGGACATCTATGCGCACGTTG 845
2y
301 IleAspAlaMetLeuGluArgMetCysHisGluGlyThrValAspIleTyrGlyHisVal 320
2y
846 ACTGTCATGTCATCAGAGAACTACATGTCGACGAGGAGCAGCAGTACGTGTTTCATC 905
2y
321 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 340
2y
906 CATTGAGCGCTGCTGGAGGCTGCAGTGGCGCCACACAGAGGTGCTGCCGCAACCTG 965
2y
341 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 360
2y
966 TATGCCCATCATCAGAGCTGGGCGCAAGTCCCTCCAGGGGAGAGTGTGACCGCATGAG 1025
2y
361 TyrAlaHisIleGlnLysLeuGlyGlnValProGlySerValThrAlaMetGlu 380
2y
1026 CTGAGTTCAAGTGTGCGGCGCTCCAGGCGCCACAGCTCCGCTTCATCAGCGCAAC 1085
2y
381 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 400
2y
1086 CTGCCCTGCAACAGTTCAAGAACCGGCTGGTGAACATCATGCCCTACGAATGACCGTT 1145
2y
401 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 420
2y
1146 GTGTGCTGTCAGCCCATCCGCTGGTGGGGCTCTGACTACATCATGCTCCAGCTTCCTG 1205
2y
421 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 440
2y
1206 GATGGTTATAGACAGAGAGGCGCTCATAGCTACACAGGGGCTCTGGCAGAGACACC 1265
2y
441 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 460
2y
1266 GAGCACTTCGGCGCATGCTATGGGACCAATTCACCATCATGCTCATGCTGACCAAG 1325
2y
461 GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLys 480
2y
1326 CTTCGGGAGATGGCAGGGGAAATGCCACAGTACTGGCAGCAGAGCGCTCTGCTCGC 1385
2y
481 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 500
2y
1386 TACAGTACTTTGTTGTTGATCCCGATGGCTGAGTACAACTGCCCGCATATCTTCGGT 1445
2y
501 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 520
2y
1446 GAGTTCAAGGTTCAGGATGCCGGGATGGGCGAGTCAAGGCAATCCGGCAGTTCCTCAGTTC 1505
2y
521 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 540
2y
1506 ACAGCTGGCCAGAGCGGCGTCCCAAGACAGGCGAGGATTCATGACTTCATCGGG 1565
2y
541 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 560
2y
1566 CAGTGTGCTAGACAGGAGCAGTTGGACGATGGCTATCAGGTCGACTGCAGT 1625
2y
561 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 580
2y
1626 GCTGCGTGGCGCCAGCGGGTGTTCATCTCTGAGCATCGCTCGAGCGCATCGC 1685
2y
581 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 600
2y
1686 TATGAGGCGTGGTGCATCTTTTCAGACCGTGAAGCCCTGGCGTACACAGCGTCCGTC 1745
2y
601 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 620
2y
1746 ATGGTGCAGACAGGACAGTATCAGTGTGCTACCGTGGCGGCTGGAGTACCTCGC 1805
2y
621 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 640
2y
1806 AGCTTTGACCACTATGCAACG 1826
2y
641 SerPheAspHisTyrAlaThr 647

RESULT 4

AAU14379
ID AAU14379 standard; protein; 647 AA.
XX
AC AAU14379;

XX 24-OCT-2001 (first entry)

XX Human novel protein #250.

XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
XX immunomodulatory; cytostatic; neuroprotective; vulnary; nootropic;
XX anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;
XX antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
XX thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
XX Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
XX tissue regeneration; immune disorder.

XX Homo sapiens.

XX WO200155437-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US002623.

XX 25-JAN-2000; 2000US-00491404.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI: 2001-451939/48.

XX N-PSDB; AAS22684.

XX Isolated polypeptides useful for treating anti-inflammatory diseases,
XX nervous system disorders, and for regenerating bone and cartilage.

XX Example 4; Page 792-793; 894pp; English.

XX The invention relates to polynucleotides encoding novel human proteins or
XX their active domains. The polypeptides, polynucleotides and antibodies
XX raised against the polypeptides are used in a method of treatment of a
XX mammal and prevention of disorders caused by the aberrant protein
XX expression or activity. The polypeptides can be used as molecular weight
XX markers, food supplements, and in antibody production. The polypeptides
XX are used to identify compounds which bind to the polypeptides.
XX Polynucleotides of the invention are used as probes and primers, for
XX sequencing, for chromosome or gene mapping, in the production of
XX recombinant proteins, and in generating anti-sense DNA or RNA and in gene
XX therapy. Polypeptides of the invention can be used to target drugs to a
XX tumour, in assays to determine biological activity, to raise
XX antibodies/ elicit an immune response, to determine quantitative protein
XX levels, as tissue markers, and to isolate receptors or ligands.
XX Polypeptides of the invention may also be useful in treating platelet
XX disorders, stem cell disorders, regenerating bone, cartilage, tendon,
XX ligament and/or nerve tissue, wound healing, treating burns, promoting
XX the proliferation, differentiation and survival of stem cells, as a
XX contraceptive, treating osteoporosis and osteoarthritis, anaemia,
XX Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
XX sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
XX fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
XX versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
XX diseases, nervous system disorders, and infection. The present sequence
XX represents a protein of the invention

XX Sequence 647 AA;

Alignment Scores:

Pred. No.: 0 Length: 647
Score: 607.00 Matches: 607
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 53.34% Indels: 0
 DB: 4 Gaps: 0

US-09-719-272-1 (1-3467) x AAU14379 (1-647)

6 GGACTGAAGGACTCTCTGCTGGCCCACTCTCTGACCTGTGAGATGCGGAGCTCAAC 65
 Db 41 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgLeuAsn 60
 Qy 66 TACAGACCCAGGATGCGAGACACCCACCCATCCCATCCATCCAGCTGGCGGCAAC 125
 Db 61 TyrGlnThrProGlyMetArgAspHisProProPheProIleThrAspLeuAlaAspAsn 80
 Qy 126 ATCGAGCCCTCAAAGCAAAGATGGCTCAAGTCTCTCCAGGAGTATGAGTCCATCGAC 185
 Db 81 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 100
 Qy 186 CTGAGACAGCAGTTCACGTGGAGAAATCAACCTCGAGGTGAACAAGCCCAAGACCCG 245
 Db 101 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 120
 Qy 246 TATCGGAATGTCATCGCTACGACCACTCTCGAGTCATCTTACTCTATCGATGGCGTC 305
 Db 121 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 140
 Qy 306 CCGGGAGTGACTACATCAATGCCCACTACATCGATGCTACCGCAAGCAGAGATGCCTAC 365
 Db 141 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 160
 Qy 366 ATCGCCAGCAGCGGCCCTCGCCGAGACCACTGGCGGATTTCTGGAGAATGGTGGGAA 425
 Db 161 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheThrArgMetValTrpGlu 180
 Qy 426 CAGCGCAGCGGCACCTGTGTCTATGATGACACGGCTGGAGGAGAGTCCCGGTAAATGT 485
 Db 181 GlnArgThrAlaThrValValMetMetThrArgLeuGluGluLysSerArgValLysCys 200
 Qy 486 GATCAGTACTGCGCAGCGGTGGCCGAGACCTGTGGCTTATTCAGTGCACCTGTG 545
 Db 201 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 220
 Qy 546 GACACAGTGGAGCTGGCCACATACACTGTGGCCACCTTCGCACCTCCACAAGAGTGGCTCC 605
 Db 221 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 240
 Qy 606 AGTGAAGACGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665
 Db 241 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 260
 Qy 666 GAGTACCCCAACTCCATCTCTGGCTTCTTACGACGGGTCAAGGGCTGCAACCCCTAGAC 725
 Db 261 GluTyrProThrProIleLeuAlaPheLeuArgAGValLysAlaCysAsnProLeuAsp 280
 Qy 726 GCAGGCCCATGTTGTGCACTGCGAGCGGGGGTGGCGCCGACCGCTGCTTCATCGTG 785
 Db 281 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 300
 Qy 786 ATTGATGCCATGTTGAGCGGATGAAGCAGCAGAGACGCTGCATCTATGGCCACCGTG 845
 Db 301 IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal 320
 Qy 846 ACTGATCGCATCAAGAGGAACATCACTGTTGTCAGACCGGAGGACGAGTACGTGTCATC 905
 Db 321 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 340
 Qy 906 CATGAGCGCTGCTGGAGGTGCCGTCGCGGCCACACAGAGTGTGCTCCCGCAACCTG 965
 Db 341 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 360
 Qy 966 TATGCCCCATCAAGAGTGGGCCCAAGTGCCTCCAGGGAGAGTGTGACCCCAATGGAG 1025
 Db 361 TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu 380

Qy 1026 CTCGAGTTCAAGTTGCTGGCCAGCTCCAAAGCCCAACAGCTCCCGCTTCATCAGCGCCAAC 1085
 Db 381 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 400
 Qy 1086 CTGCCCCTCAACAGTTCAAGAACCGCTGGTGAACATCATGCTCCCTCAGATTGACCGGT 1145
 Db 401 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 420
 Qy 1146 GTGTGCTCGACGCCCATCCGTGGTGTGGAGGGCTCTGACTACATCAATGCCAGTTCCTG 1205
 Db 421 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 440
 Qy 1206 GATGTTATAGACAGACAGCCCTACATGCTACACAGGGGCTCTGGCAGAGAGACACC 1265
 Db 441 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 460
 Qy 1266 GAGGACTTCTGGCGCATGCTATGGAGCACAATTCACCATCATGCTCATGCTGACCAAG 1325
 Db 461 GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLys 480
 Qy 1326 CTTGGGAGATGGGAGGAGAAATGCCACAGTACTGGCCAGCAGAGCGGCTGCTGCTGC 1385
 Db 481 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 500
 Qy 1386 TACAGTACTTTGTTGACCCGATGGCTGAGTACAAACATGCCCCAGTATATCTGCGT 1445
 Db 501 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 520
 Qy 1446 GAGTTCAAGTCAAGACCCCGGATGGCGAGTCAAGACAAATCCGCGAGTCCAGTTC 1505
 Db 521 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 540
 Qy 1506 ACAGCTGCCAGAGCAGGGCGTCCCAAGACAGCGAGGGATTTCATTGACTTCATCGGG 1565
 Db 541 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 560
 Qy 1566 CAGGTGCATAGAACCAGAGCAGTTTGAAGAGTGGCCCTATCACGTGCACTGCACT 1625
 Db 561 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 580
 Qy 1626 GCTGGCGTGGCGCCAGCGGGTTCATCTCTGAGCATGCTCTGGAGCGCATGGCC 1685
 Db 581 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 600
 Qy 1686 TATGAGGGGTGGTCACATGTTTCAGACCCGTGAAGACCTCGTACACAGCGTCTCGCC 1745
 Db 601 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 620
 Qy 1746 ATGTCGACAGACAGACCCAGTATCAGCTGTGCTACCGTGGCGCCCTGAGTACCTCGC 1805
 Db 621 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 640
 Qy 1806 AGCTTTGACCACTATGCAACG 1826
 Db 641 SerPheAspHisTyrAlaThr 647

RESULT 5

AAE37971
 ID AAE37971 standard; protein; 1796 AA.

XX AC AAE37971;

XX DT 06-NOV-2003 (first entry)

XX DE Human kinase and phosphatase (KPP-16) protein.

XX KW Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;
 KW atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;
 KW psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome;
 KW renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;
 KW neurological disorder; parkinson's disease; epilepsy; glomerulonephritis;
 KW autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;

acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; neutropenic; dermatitis; multiple sclerosis; diabetes mellitus; allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.

Homo sapiens.

WO2003050084-A2.

19-JUN-2003.

06-DEC-2002; 2002WO-US039126.

07-DEC-2001; 2001US-0340235P.

19-DEC-2001; 2001US-034007P.

21-DEC-2001; 2001US-0343546P.

04-FEB-2002; 2002US-0354388P.

15-FEB-2002; 2002US-0357675P.

(INCY-) INCYTE GENOMICS INC.

Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AB;

Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP;

Baughn MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;

Becha SD, Lee SY, Sprague WW, Zebajradian Y;

WPI; 2003-532894/50.

N-PSDB; AAD57343.

New human kinases and phosphatases and polynucleotides, useful for

diagnosing, treating or preventing autoimmune or inflammatory disorders

(e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,

cancer or hepatitis.

Claim 1; Page 216-220; 282pp; English.

The invention relates to an isolated polypeptide, which is a human kinase

and phosphatase (KPP). KPP agonists and antagonists are useful for

diagnosing, treating or preventing disorders associated with aberrant

expression of KPP, particularly cell proliferative disorders (e.g.

arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal

nocturnal haemoglobinuria, polycythaemia vera, boriasis, primary

thrombocytopaenia or cancer), developmental disorders (eg. renal tubular

acidosis, anaemia or mental retardation), neurological disorders (e.g.

Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/

inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,

allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's

disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,

gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,

multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's

syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,

bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP

is useful in assessing the effects of exogenous compounds on the

expression of nucleic acids and kinases and phosphatases. KPP gene is

useful in gene therapy and for creating transgenic animals to model human

66 TACGAGACCCAGGTATGGAGACACACCCATCCATCCAGCAGCTGGGACAC 125

1210 TyrGlnThrProGlyMetArgAspHisProPheIleThrAspLeuAlaAspAsn 1229

126 ATGAGCGCTCAAAACCAACGATGCGCTCAAGTCTCCAGAGTATGAGTCCATCGAC 185

1230 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 1249

186 CTGGAGCAGAGTTCAGTGGGAGAAATTCAACTGGAGGTGAACAAGCCCAAGACCCG 245

1250 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnAsn 1269

246 TATGCGAATGTCATCGCTACGACCACTCTCGAGTCACTTACCTCTCTATCGATGGCGTC 305

1270 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1289

306 CCGGAGTCACTACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 365

1290 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1309

366 ATGCGCAGCAGGCGCCCTGCGGAGACCACTGGGAGATTTCTGGAGAAATGGTGGAA 425

1310 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheIleArgMetValTrpGlu 1329

426 CAGCGCAGCGCCCACTGTGTGTCATGATGACACCGCTGGAGAGAGTCCCGGTAAATGT 485

1330 GlnArgThrAlaThrValValMetMetThrArgLeuGluLysSerArgValLysCys 1349

486 GATCAGTACTGGCGCGCCCTGCGGAGACCACTGGGAGATTTCTGGAGAAATGGTGGAA 545

1350 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 1369

546 GACACAGTGGAGCTGGCGCCCACTGTCGACATCACTGTCGACCTCCACCAAGAGTGGCTCC 605

1370 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 1389

606 AGTGAGAGCGTGGAGTGGCTGAGTTCAGTTCATGGCTGGCGGAGACCACTGAGTTCCT 665

1390 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaIleProAspHisGlyValPro 1409

666 GAGTACCCAACTCCCATCTCCCTGCGCTTCTTACGAGCGGTCAAGGCTGCAACCCCTAGAC 725

1410 GluTyrProThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAsp 1429

726 CGAGCGCGCCCACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 785

1430 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1449

786 ATTGATGCGCATGTTGGAGCGGATGAGACGAGACGAGACGAGACGAGACGAGACGAG 845

1450 IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal 1469

846 ACCTGCGATGCGATCAGAGAGAACTACATGTCGAGACGAGACGAGACGAGACGAGACG 905

1470 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 1489

906 CATGAGCGCTGCTGGAGGCTGCCACGTCGCGGACACACAGAGGTGCTGCCCGCAACCTG 965

1490 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 1509

966 TATGCCACATCCAGAGCTGGCGCAAGTGCCTCCAGGAGAGTGTGACCGCATCGAG 1025

1510 TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu 1529

1026 CTCGAGTTCAGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1085

1530 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1549

1086 CTGCGCTCCAAACAAAGTTCAGAGACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1145

1550 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1569

Alignment Scores:
Pred. No.: 0 Length: 1796
Score: 607.00 Matches: 607
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.34% Indels: 0
Gaps: 6

US-09-719-272-1 (1-3467) x AA637971 (1-1796)

2y 6 GGATGAGAGACTCTGCTGGCGCATCTCTGACCTCTGAGAGTGGAGGCTCAAC 65

2b 1190 GlyLeuLysAspSerLeuLeuAlaHisSerAspProValGluMetArgLeuAsn 1209

QY 1146 GTGTGCTGAGCCCATCGTGTGTGGAGGCTCTGACTACATCAATGCGAGCTTCCTG 1205
Db 1570 ValCysLeuGlnProIleAsglyValGluGlySerAspTyrIleAlaSerPheLeu 1589
QY 1206 GATGGTTATAGACAGAGAAGGCTCATAGCTACACAGGGGCTCTGGCAGAGACACC 1265
Db 1590 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 1609
QY 1266 GAGACTTCTGGCCATGCTATGGAGACAAATCCACCATCATCGTCATGCTGACCAAG 1325
Db 1610 GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleValMetLeuThrLys 1629
QY 1326 CTTCCGAGATGGCAGGAGAAATGCCAGTACTGGCAGAGCCCTCTGCTGCG 1385
Db 1630 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 1649
QY 1386 TACAGACTTTGTTGTCACCCATGCTGAGTACAACTGCCCCAGTATATCTTCGCT 1445
Db 1650 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 1669
QY 1446 GAGTTCAAGGTCAAGGATGCCCGGATGGGAGTCAAGGACAATCCGGCAGTTCCAGTTC 1505
Db 1670 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleAsgGlnPhe 1689
QY 1506 ACAGACTGGCAGAGCGGCTGCCAGACAGCGAGGATTCATGACTTCATCGCG 1565
Db 1690 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1709
QY 1566 CAGGTGCATAGACACAGGAGCAGTTTCGACAGATGGGCTATCGAGTGCACCTGCAGT 1625
Db 1710 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1729
QY 1626 GCTGGCGTGGCGGACCGGGGTTCATCTGACTGACATCGCTCGGAGCGATCGC 1685
Db 1730 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1749
QY 1686 TATGAGGCGTGTGCGACATGTTTCAGACCGTGAAGACCTGCGTACACAGCGTCTGCC 1745
Db 1750 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuAsgThrGlnArgProAla 1769
QY 1746 ATGGTGCAGACAGAGCACAGTATCAGTGTGCTACCTGCGGCGCTGGAGTACTCGGC 1805
Db 1770 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 1789
QY 1806 AGCTTTGACCATGTCACAG 1826
Db 1790 SerPheAspHisTyrAlaThr 1796
RESULT 6
ID AAY81785
AC AAY81785 standard; protein; 1897 AA.
XX AAY81785;
AC AAY81785;
XX 07-JUN-2000 (first entry)
XX Human protein tyrosine phosphatase, LAR, protein sequence.
DE
XX
XX Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR;
KW CD45; PTP; diagnosis; insulin resistance related disease; syndrome X;
KW non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;
KW heart disorder.
XX
OS Homo sapiens.
XX
PN WO200002922-A1.
XX
PD 20-JAN-2000.
XX
PF 06-JUL-1999; 99WO-JP003656.
XX
PR 10-JUL-1998; 98WO-JP003120.
XX

(FUSO) FUSO PHARM IND LTD.
XX Yamamoto H, Tsujikawa K, Uchino Y;
PI N-PSDB; AA291908.
XX WPI; 2000-182215/16.
DR N-PSDB; AA291908.
XX
PT Antibody for diagnosis and treatment of insulin resistance disorders and
syndrome X recognises the intracellular domains of tyrosine kinases.
PS Example 1; Page 61-77; 83pp; Japanese.
XX This sequence is the protein tyrosine phosphatase LAR. The invention
relates to an antibody specifically recognising the intracellular domains
of two or more protein tyrosine phosphatases (PTP). The antibody is
useful for the detection and assay of PTP including novel phosphatases
generated by cloning; and diagnosis, treatment and prevention of insulin
resistance related diseases and non-insulin dependent diabetes mellitus,
syndrome X and arteriosclerosis and heart disorders
XX Sequence 1897 AA;
SQ
Alignment Scores:
Pred. No.: 0 Length: 1897
Score: 607.00 Matches: 607
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.34% Indels: 0
DB: 3 Gaps: 0
US-09-719-272-1 (1-3467) x AAY81785 (1-1897)
QY 6 GGACTGAAGGACTCTGTGCTGCCCATCTCTGTACCTGTGGAGATCGGAGGCTCAAC 65
Db 1291 GlyLeuLysAspSerLeuAlaHisSerSerAspProValGluMetArgArgLeuAsn 1310
QY 66 TACAGACCCAGGTATGCGAGACACACCCATCCCATCCAGCTCGCGGAGAAC 125
Db 1311 TyrGlnThrProGlyMetArgAspHisProIleThrAspLeuAlaAspAsn 1330
QY 126 ATCGAGCGCTCAAGCCCAACAGTGCCTCAAGTTCTCCAGGAGTATGAGTCCATCCAC 185
Db 1331 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGlyTyrGluSerIleAsp 1350
QY 186 CTTGGACAGCAGTTCACTGGGAGAAATCAAACCTGGAGGTGAACAAGCCAGAACCGC 245
Db 1351 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 1370
QY 246 TATGCAATGTCTATCGCTTACGACCATCTCGAGTCATCTTACCTCTATCGATCGCGTC 305
Db 1371 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1390
QY 306 CCGGAGTGACTACATCAATGCCAACTACATCGATGGCTACCGAAGCAGAAATGCTTAC 365
Db 1391 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1410
QY 366 ATGCGCAGCAGGCGCCCTGCGGAGACCATGCGGATTTCTGGAGATGCTGTGGGAA 425
Db 1411 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu 1430
QY 426 CAGCGACAGCGCCACTGCTGCTCATGATGACACCGCTGGAGGAGAGTCCCGGTAAATGT 485
Db 1431 GlnArgThrAlaThrValValMetMetThrArgLeuGluLysSerArgValLysCys 1450
QY 486 GATCAGTACTGGCCAGCGCTGGCCAGACCTGTGGCTATTTCAGGTGACCTGTGTG 545
Db 1451 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 1470
QY 546 GACACAGTGAGCTGGCCACATACACTGTGCGCACCTTCGCTCTCCACAGAGTGGCTCC 605
Db 1471 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 1490
QY 606 AGTGAGAACGCTGAGCTGGCTGCTTTCATGTTTCATGCTGCTGCTGCTGCTGCTTCT 665

1491 SerGluYsArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1510
666 GAGTACCAACTCCCAATCTGGCTTCCTACGAGCGGTCAAGCGCTGCAACCCCTAGAC 725
1511 GluTy-ProThrProIleLeuAlaPheLeuArgValValysAlaCysAsnProLeuAsp 1530
726 GCAGGCGCATGGTGTGCACTCAGCGGGGGTGGCGGACCGGCTGCTTCATCGTG 785
1531 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1550
786 ATGTATGCCATGTGGAGCGGATGAAGACGAGACGAGCGGTGACATCTATGCCACGTG 845
1551 IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrgLysHisVal 1570
846 ACCTGATCGATCAGACAGAGAACTCATGTCACAGCGGAGGACGACGACGTGTTTCATC 905
1571 ThrCysMetArgSerGlnArgAsnTyrgMetValGlnThrGluAspGlnTyrgValPheIle 1590
906 CATGAGCGCTGCTGGAGGTGCCACGTGGCCACACAGAGGTGCTGCCCGCAACCTG 965
1591 HisGluAlaLeuLeuGluAlaIleThrCysGlyHisThrGluValProAlaArgAsnLeu 1610
966 TATGCCCATCAGACAGCTGGCGCAAGTCCCTCAGGGGAGGTGACCGCCATGGAG 1025
1611 TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu 1630
1026 CTGAGTTCAAGTTGCTGGCGAGCTCAAGCGCCACACGCTCCCGCTTCATCAGCGCCAC 1085
1631 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1650
1086 CTGCGCTGCAAGTTCAAGACCGGCTGGTGAACATCATGCTCATCATGCTTCCTG 1145
1651 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrgLysLeuThrArg 1670
1146 GTGTGCTGTCAGCCCATCGTGTGGAGGCTCTGACTACATCATCATGCTTCCTG 1205
1671 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrgIleAsnAlaSerPheLeu 1690
1206 GATGGTTATAGACAGAGAGGCTCATAGCTACACAGGGGCTCTGGCAGAGACAC 1265
1691 AspGlyTyrgGlnGlnLysAlaTyrgIleAlaThrGlnGlyProLeuAlaGluSerThr 1710
1266 GAGGACTTCTGGCGCATGCTATGGAGACAAATCCACCATCATGCTCATGTCGACCAAG 1325
1711 GluAspPheIrgMetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLys 1730
1326 CTTCGGAGATGGCAGGAGAAATGCCACGATCTAGCTACACAGGGGCTCTGGCAGAGACAC 1385
1731 LeuArgGluMetGlyArgGluLysCysHisGlnTyrgTrpProAlaGluArgSerAlaArg 1750
1386 TACCAGTACTTGTGTGACCGCATGGCTGAGTACACATGCTCATGCTCATGCTTCCTGCT 1445
1751 TyrGlnTyrgPheValValAspProMetAlaGluTyrgAsnMetProGlnTyrgIleLeuArg 1770
1446 GAGTTCAAGTTCAGGATGCGCGGATGGCAGTCAAGGACAAATCCGGCAGTTCCAGTTC 1505
1771 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
1506 ACAGACTGGCCAGAGAGGGGCTGCCAAGCAGCGGAGGATTCATGACTTCATCGGG 1565
1791 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1810
1566 CAGGTGATAGACCAAGGAGCAGTTTGGACGAGATGGGCTCATCAGGTGCACTGCAGT 1625
1811 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1830
1626 GCTGGGTGGCGCCGACCGGGGTGTTTATCTCTGAGCATCTGCTGGAGCGCATCGGC 1685
1831 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1850
1686 TATCAGGCGGTGGTGCATGTTTCAGACCGTGAAGACCGCTGCATACAGCGCTCTGCC 1745

1851 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1870
1746 ATGTGTGAGACAGAGGACAGTATCAGCTGTGTACCGTGGCGCTCGAGTACCTCGGC 1805
1871 MetValGlnThrGluAspGlnTyrgLeuLeuCysTyrgAlaAlaLeuGluTyrgLeuGly 1890
1806 AGCTTTCACCACTATGCAACG 1826
1891 SerPheAspHisTyrgAlaThr 1897
RESULT 7
AAY56100
ID AAY56100 standard; protein; 1897 AA.
XX
AC AAY56100;
XX
DT 17-APR-2000 (first entry)
XX
DE LAR tyrosine phosphatase.
XX
KW Intracellular domain; P-subunit; human; leucocyte antigen related; LAR;
KW tyrosine phosphatase; antibody; thyroid cancer.
XX
OS Homo sapiens.
XX
PN WO9964591-A1.
XX
PD 16-DEC-1999.
XX
PF 07-JUN-1999; 99WO-JP003054.
XX
PR 08-JUN-1998; 98WO-JP002542.
XX
PA (FUSO) FUSO PHARM IND LTD.
XX
PI Yamamoto H, Tsujikawa K, Uchino Y, Konishi N;
XX
DR WPI; 2000-097539/08.
DR N-PSDB; AAZ59133.
XX
PT Antibody recognizing the intracellular domain of the human tyrosine
phosphatase LAR.
XX
PS Disclosure; Page 81-97; 104pp; Japanese.
XX
CC This sequence represents the complete human leucocyte antigen related
(LAR) tyrosine phosphatase. The invention relates to the generation of an
antibody recognizing the intracellular domain of the human LAR tyrosine
phosphatase (AAY56098). The antibody is used for the diagnosis and
treatment of thyroid cancer
XX
SQ Sequence 1897 AA;
Alignment Scores:
Pred. No.: 0 Length: 1897
Score: 607.00 Matches: 607
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.34% Indels: 0
DB: 3 Gaps: 0
US-09-719-272-1 (1-3467) x AAY56100 (1-1897)
QY 6 GAGTGAAGGACTCTTCTGCTGGCCACTCTCTGACCTGTGGAGATCGGAGGCTCAAC 65
DB 1291 GlyLeuLysAspSerLeuAlaHisSerSerAspProValGluMetArgLeuAsn 1310
QY 66 TACCAGACCCAGAGTATCGGAGACCAACCCATCCCATCCAGCTCGGCGGACCAAC 125
DB 1311 TyrGlnThrProGlyMetArgAspHisProIleThrAspLeuAlaAspAsn 1330
QY 126 ATCGAGCGCTCAAGACCAACGATGGGCTCAAGTCTCCAGAGGTATGATCCATCGAC 185

1331 IleGluArgLeuLeuYsAlaAsnAspGlyLeuYsPheSerGlnGluTyrGluSerIleAsp 1350
186 CQTGGACAGCAGTTCACGTGGGAGAAATCAACCTGGAGGTGAACAGCCAGACCCG 245
1351 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 1370
246 TATCGGAATGTCATCGCTCAGCAGCACTCTCGAGTCATCTTACTCTATCGATGGCGTC 305
1371 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1390
306 CCGGGAGTGACTACATCAATGCGCAACTACATCATGCTTACCGCAGCAGAGATGCCCTAC 365
1391 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1410
366 ATCGCCAGCAGGCGCCCTCCCGAGACCATGGCGCATTTCTGGCAATGGTGTGGGAA 425
1411 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu 1430
426 CAGCGCACGGCCATCGTTCATGATGATGACACGGCTGGAGGAGAGTCCCGGGTAAATGT 485
1431 GlnArgThrAlaThrValValMetMetThrArgLeuGluGluYsSerArgValLysCys 1450
486 GATCAGTACTGGCCAGCGGTGGACCGAGACCTGTGGCCTTATTTCAGGTGACCTGTG 545
1451 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 1470
546 CACACAGTGGAGCTGGCCACATACACTGTGGCCACCTTCGCACATCCCAAGAGTGGCTCC 605
1471 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 1490
606 AGTGAGAGCGTGACTGGCTGAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 665
1491 SerGluYsArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1510
666 GAGTACCACTCCCATCTCTGGCCCTCTTACGACGGGTCAAGGGCTGCAACCCCTAGAC 725
1511 GluTyrProThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAsp 1530
726 GAGGGCCCATGGTGGTGCATGACGCGCGGTGGCGCCGCGCTGCTTCATCGTG 785
1531 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1550
786 ATTGATGCATCTGGAGCGGTGAAGCAGCAGAGAGCGGTGGACATCTATGGCCAGCTG 845
1551 IleAspAlaMetLeuGluArgMetLysHisGluYsThrValAspIleTyrGlyHisVal 1570
846 ACTGATCGCATCAGAGAACTACATGTGTGCAGACGGAGACCCAGTACGTGTTCATC 905
1571 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 1590
906 CATGAGGCGCTCTGGAGCTCCAGCTCGCGCCACACAGAGTGCCTCGCCGCAACCTG 965
1591 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 1610
966 TATGCCCATCATCAGAACTGGGCCAAGTGCCTCCAGGGGAGAGTGTACCGCCATGGAG 1025
1611 TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu 1630
1026 CTCGAGTTCAGTTCGTGGCTCCAGGCGCCACAGCTCCCGTTCATCAGCGCCCAAC 1085
1631 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1650
1086 CTGCCCTGCAACAAAGTTCAGAACCGGCTGGTGAACATCATCCCTACGAATGACCGCT 1145
1651 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1670
1146 GTGTGTCTGAGCCCATCGTGTGGTGGAGGCTCTGACTACATCAATGCCAGCTTCCTG 1205
1671 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 1690
1206 GATGGTTATAGACAGCAGAGGCTTACATAGCTTACACAGGGGCTCTGCGCAGAGACCC 1265
1691 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 1710

1266 GAGGACTTCTGGCGCATGCTATGGAGCACAATTCACCATCATCGTCACTGCTACCAAG 1325
1711 GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLys 1730
1326 CTTCCGGAGATGGGAGGAGAAATGCCACAGTACTGGCCAGCAGAGCGCTCTGCTCGC 1385
1731 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 1750
1386 TACCAGTACTTGTGTGGTGGCCGATGGCTCAGTACACATGCCCAAGTATATCTCGCT 1445
1751 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 1770
1446 GAGTTCAAAGGTCAACGATGCCCGGATGGCAGTCAAGGACCAATCCGGCAGTTCAGTTC 1505
1771 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
1506 ACAGACTGGCCAGACAGCGGTGGCCCAAGACAGCGAGGAGTTCATTGACTTCATCGGG 1565
1791 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1810
1566 CAGGTGCATTAAGACCAAGAGCAGTTCGACAGGATGGGCTTATCACCGTGCATGCACT 1625
1811 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1830
1626 GCTGGCTGGCGCGCAGCGGTGGTTCATCTGAGCATCGTCTCGAGCGCATGCGC 1685
1831 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1850
1686 TATGAGGGCTGGTTCGACATGTTTCAGACCGGTGAAGACCTCGGTACACAGCGTCTGCC 1745
1851 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1870
1746 ATGGTCCAGACAGAGACCGATCAGCTGCTGCTACCGTGGCGCTCGAGTACCTCGCGC 1805
1871 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaLeuGluTyrLeuGly 1890
1806 AGCTTTGACCACTATGCAACG 1826
1891 SerPheAspHisTyrAlaThr 1897
RESULT 8
ID AAB19712 standard; protein; 1897 AA.
XX AAB19712;
XX 19-FEB-2001 (first entry)
XX Human protein tyrosine phosphatase PAP LAR.
XX PTP LAR; protein tyrosine phosphatase; leukocyte antigen related; human;
XX epithelial cell; cell migration; cell proliferation; cancer; antitumour;
XX metastasis; antimetastatic; wound healing; vulnery; diagnosis; therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..16
FT /label= Signal_peptide
FT Protein 17..1897
FT /label= Mature_protein
FT Domain 37..99
FT /label= Immunoglobulin_domain
FT Domain 139..199
FT /label= Immunoglobulin_domain
FT Domain 236..290
FT /label= Immunoglobulin_domain
FT Domain 309..391
FT /label= Fibronectin-type-III_domain
FT Domain 403..490
FT /label= Fibronectin-type-III_domain
FT Domain 502..584

T Domain /label= Fibronectin-type-III_domain
 T 596..696
 T /label= Fibronectin-type-III_domain
 T 698..799
 T /label= Fibronectin-type-III_domain
 T 811..894
 T /label= Fibronectin-type-III_domain
 T 905..990
 T /label= Fibronectin-type-III_domain
 T 1365..1596
 T /label= Protein-tyrosine_phosphatase

T X WO200061180-A2.

T X 19-OCT-2000.

T X 06-APR-2000; 2000WO-US009274.

T X 09-APR-1999; 99US-0128673P.

T X (PLAC) MAX PLANCK INST.

T X Ullrich A, Muller T;

T X WPI; 2000-647399/62.

T X N-PSDB; AAA88739.

T Treating a disease or a disorder characterized by epithelial cell
 T migration comprises administering a pharmaceutically acceptable
 T composition comprising PTP LAR.

T X Disclosure; Fig 9; 107pp; English.

T X The present sequence is that of human protein tyrosine phosphatase PTP
 T LAR (leukocyte antigen related), a negative regulator of epithelial cell
 T migration and tumour formation, for which beta-catenin is a substrate. A
 T dysfunction of PTP LAR may lead to tumour invasion and metastasis. The
 T invention provides methods for diagnosing, preventing, or treating a
 T disease or disorder characterized by epithelial cell migration, increased
 T tyrosine phosphorylation of beta-catenin, and/or increased levels of the
 T pool of free beta-catenin, especially cancer, metastasis and aberrant
 T wound healing (claimed). The methods may also be used to treat diseases
 T and disorders with abnormal cell proliferative conditions, including
 T fibrotic and mesangial disorders, abnormal angiogenesis and
 T vasculogenesis, psoriasis, diabetes mellitus and inflammation. Methods
 T are provided for identifying compounds that modulate PTP LAR activity for
 T use in treatment

T X Sequence 1897 AA;

T X Alignment Scores:

T X Pred. No.: 0 Length: 1897
 T X Score: 607.00 Matches: 607
 T X Percent Similarity: 100.00% Conservative: 0
 T X Best Local Similarity: 100.00% Mismatches: 0
 T X Query Match: 53.34% Indels: 0
 T X DB: 3 Gaps: 0

US-09-719-272-1 (1-3467) x AAB19712 (1-1897)

QY 6 GGACTGAAGNCTCTTGCTGGCCCATCTCTGACCCCTGTGGAGTGGCGGCTCAAC 65
 Db 1291 GlyLeuLysAspSerLeuLeuAlaHisSerAspProValGluMetArgArgLeuAsn 1310
 QY 66 TACCAGACCCAGGTATGCGAGACACCCACCCATCCCGACCTGGCGGCAAC 125
 Db 1311 TyrGlnThrProGlyMetArgAspHisProProlleThrAspLeuAlaAspAsn 1330
 QY 126 ATCGAGCGCCTCAAGCAACGATGGCTCAGTCTCCAGGAGTATGATCCATCGAC 185
 Db 1331 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 1350
 QY 186 CTGGACAGCAGTTCACGTGGGAGATTCAAACCTGGAGGTGAACAAGCCCAAGACCGC 245

Db 1351 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 1370
 QY 246 TATGCGAATGTCATCGCTACGACCACTCTCGAGTCACTTACCTCTATCGATGCGCTC 305
 Db 1371 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1390
 QY 306 CCGGGAGTGACTACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 365
 Db 1391 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1410
 QY 366 ATGCGCACGCGAGCGCCCTGCGCGAGACCACTTCTGGAGAATGGTGTGGGAA 425
 Db 1411 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu 1430
 QY 426 CAGCGCACGCGCACTGTGTGATGACACGCGCTGGAGAGAGTCCCGGTTAAATGT 485
 Db 1431 GlnArgThrAlaThrValValMetMetThrArgLeuGluGluLysSerArgValLysCys 1450
 QY 486 GATCAGTACTGGCGCGCTGCGCGAGACCACTGTGGCTTATTTCAGGTGACCTGTGTG 545
 Db 1451 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 1470
 QY 546 GACACAGTGGAGTGGCCACATACATCTGTGCGCACTTGTGCACTCCACAGAGTGGTCC 605
 Db 1471 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 1490
 QY 606 AGTGAGAGGTGAGTGGCTCAGTTTCAGTTTCAGTTTCAGTTTCAGTTTCAGTTTCCT 665
 Db 1491 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1510
 QY 666 CAGTACCCCACTCCCATCTCTGCGCTTCTACGCGGTCAAGGCTGCAACCCCTAGAC 725
 Db 1511 GluTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 1530
 QY 726 CGAGGCGCCATGTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 785
 Db 1531 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1550
 QY 786 ATTGATGCGATTTGGAGCGGATGAAGCAGAGAGACGCTGACATCTATGCGCACGTG 845
 Db 1551 IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal 1570
 QY 846 ACCTGCTATGCGATCACAGAGAACTACATGTTGTCAGACGAGAGACGAGTGTTCATC 905
 Db 1571 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 1590
 QY 906 CATGAGCGCTGCTGGAGGCTGCCACGTGGCGGCACACAGAGGTGCTGCGCGCAACCTG 965
 Db 1591 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 1610
 QY 966 TATGCCCATCCAGAACTGGCCAAAGTGGCTCCAGGGAGAGTGTACCGCCATGAG 1025
 Db 1611 TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu 1630
 QY 1026 CTCGAGTTCAAGTGTGCGCCAGCTCCAAAGCCACACAGTCCCGCTTCATCAGCGCCAAC 1085
 Db 1631 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1650
 QY 1086 CTGCGCTGCAACAAGTTCAGAACCGCTGTGTGATCATATGCTCCCTACGATTCACCGCT 1145
 Db 1651 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1670
 QY 1146 GTGTGCTGCGCCCATCCGCTGCTGAGGGCTGTGACTACATCAATGCCAGTCTCTCTG 1205
 Db 1671 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 1690
 QY 1206 GATGTTTATAGACAGCAGAAGCCCTACATAGCTACACAGGGGCTCTGGCAGAGACCC 1265
 Db 1691 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 1710
 QY 1266 GAGGACTTCTGGCGATGCTATGGAGACCAATCCACCATCGTCTCATCTGACCAAG 1325

Db 1711 GluAspPheTrpArMetLeuTrpGluHisAsnSerThrIleValMetLeuThrLys 1730
Qy 1326 CTTGGAGATGGCGAGGAAATGCCACAGTACTGGCCAGCAGCGCTCTGCTGC 1385
Db 1731 LeuArgGluMetGlyA:gglyuCyHisGlnTrpProAlaGluArgSerAlaArg 1750
Qy 1386 TACCAGTACTTTGTTGTTGACCCCATGGCTGAGTACACATGCCGCCAGTATATCTCGGT 1445
Db 1751 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 1770
Qy 1446 GAGTTCAAGTACAGATGCCCGGATGGGAGTCAAGGCAATCCGGCAGTTCAGTTC 1505
Db 1771 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
Qy 1506 ACAGACTGCCAGACAGCGCGTGTCCCAAGACAGCGGAGGATTCATTGACTTCATCGCG 1565
Db 1791 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1810
Qy 1566 CAGGTGCATAGACACAGACAGTTCGACAGATGGGCTATCAGGTGCAGTGCAGT 1625
Db 1811 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1830
Qy 1626 GTGCGCGTGGCGCGCACCGCGTGTTCATCTCTGAGCATCGTCTCGAGCGCATCGCG 1685
Db 1831 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1850
Qy 1686 TATGAGCGGTGGTGCAGATGTTTCAGACCGGTGAGACCCCTGCTACACAGCGTCTGCC 1745
Db 1851 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1870
Qy 1746 ATGGTGCAGACAGAGACAGTATCAGTGTGCTACCGTGGCGGCTCGGAGTACCTCGCG 1805
Db 1871 MetValGlnThrGluAspGlnTyrGlnLeuGlyCysTyrArgAlaAlaLeuGluTyrLeuGly 1890
Qy 1806 AGCTTTGACCACTATGCAACG 1826
Db 1891 SerPheAspHisTyrAlaThr 1897
RESULT 9
ID ADD18740 standard; protein; 1897 AA.
AC ADD18740;
DT 15-JAN-2004 (first entry)
DE Human disease related protein SeqID171.
XX human; disease state; cytostatic; antiinflammatory; ophthalmological;
KW antiarteriosclerotic; vulnary; gene therapy;
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW glucose transportation; catecholamine synthesis; iron transport;
KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW inflammatory condition; wound healing.
XX Homo sapiens.
XX WO2003018621-A2.
XX 06-MAR-2003.
XX 23-AUG-2002; 2002WO-GB003892.
XX 23-AUG-2001; 2001GB-00020558.
XX 05-OCT-2001; 2001GB-00024037.
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX Kingman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
XX WPI; 2003-290046/28.

DR N-PSDB; ADD18741.
XX New substantially purified polypeptide, useful for diagnosing or treating
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
PT wound healing.
XX Claim 25; SEQ ID NO 171; 424pp; English
PS
XX This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory, the
CC ophthalmological, antiarteriosclerotic or vulnary activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein of the invention.
XX Sequence 1897 AA;

Alignment Scores:
Pred. No.: 0 Length: 1897
Score: 607.00 Matches: 607
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.34% Indels: 0
DB: 7 Gaps: 0

US-09-719-272-1 (1-3467) x ADD18740 (1-1897)

Qy 6 GGACTAAGAGTCTCTGTGCTGCCCATCTCTGTGACCTGTGGAGATGGGAGCTCAAC 65
Db 1291 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgArgLeuAsn 1310
Qy 66 TACCAGACCCAGGTATGGAGACACCCACCCATCCCATCCCATCCAGGAGTATGAGTCCATGCAC 125
Db 1311 TyrGlnThrProGlyMetArgAspHisProProlIleProlIleThrAspLeuAlaAspAsn 1330
Qy 126 ATCGAGCGCTCAAGCCCAACGATGGCTCAAGTTCCTCCAGGAGTATGAGTCCATGCAC 185
Db 1331 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 1350
Qy 186 CTTGGACAGCAGTTCACGTGGGAGATTCACACCTGGAGGTGACCAAGCCCAAGAACCGC 245
Db 1351 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 1370
Qy 246 TATGCGAATGTCACTGCCCTACGACCACTCTCGAGTCACTCTTACCTCTATCGATGGCTC 305
Db 1371 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1390
Qy 306 CCGGGAGTGACTACTATCCCACTACATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 365
Db 1391 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1410
Qy 366 ATGCCACGACGAGCGCCCTCCCGGAGACATGGCGGATTTCTGGAGATGGTGGGAA 425
Db 1411 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu 1430
Qy 426 CAGGCGACGCGCTCTGTGTCATGATGACACCGCTGGAGGAGAGTCCGGGTAAATCT 485
Db 1431 GlnArgThrAlaThrValMetMetThrArgLeuGluGluLysSerArgValLysCys 1450
Qy 486 GATCAGTACTGCGCAGCCCGTGGCAGACCTGTGGCTTATTCAGGTGACCTGTG 545
Db 1451 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 1470
Qy 546 GACACAGTGAGCTGGCCACATACATCTGTGGCACCTTGGCACTCCACAGAGTGGCTCC 605

1471 AspThrValGluLeuAlaThrThrValArgThrPheAlaLeuHisLysSerGlySer 1490
606 AGTGAGAGCGTGAGTGGCTCAGTTTCAGTTTCATGGCTGGCCAGACCATGAGTTCT 665
1491 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1510
666 GAGTACCACCACTCCATCCGCTTCCCTACGAGGAGTCAAGGCTGCAACCCCTAGAC 725
1511 GluTrpProThrProLeuLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 1530
726 GCAGGCGCCATGTGTGCTACTCAGCGGGGCTGGCGCCAGACCGCTGCTTCATCGTG 785
1531 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1550
786 ATTGATGCGCATGTGGCGGATGAGCAGCAGACGAGCGTGGACATCTATGCCACGCG 845
1551 IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleThrGlyHisVal 1570
846 ACCTGATGCGATCAGAGAGAACTACATGCTGCAGACGAGGAGCAGTACGTTTCATC 905
1571 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 1590
906 CATGAGCGCTGCTGGAGCTGCACGTGGCGCCACACAGAGGTGCTGCCGCAACCTG 965
1591 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 1610
966 TATGCCACATCAGAGCTGGCGCAAGTCCCTCCAGGGGAGAGTGTGACCGCATGAG 1025
1611 TyrAlaHisGluGlnLysGluValProProGlyLysSerValThrAlaMetGlu 1630
1026 CTGAGTTCAAGTGTGGCGAGCTCAAGGCCACACGTCCTCCGCTTCATCGCGCCAC 1085
1631 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1650
1086 CTGCGCTGCAACAGTTCAAGAACCGCTGCTGAAATCATCATGCTCCCTACGAATTCAC 1145
1651 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1670
1146 GTGTGTCTGAGCCCATCCGTGTGTGGAGGCTCTGACTACATCATGATGCGCTTCCTG 1205
1671 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 1690
1206 GATGGTTATAGACAGAGAGGCTACATAGCTACACAGGGGCTCTGGCAGAGAGCACC 1265
1691 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 1710
1266 GAGGACTTCTGGCGCATGCTATGGAGACCAATCCACCATCATGCTCATGCTGACCAAG 1325
1711 GluAspPheThrArgMetLeuTrpGluHisAsnSerThrIleValMetLeuThrLys 1730
1326 CTTCCGAGATGGCAGGAGGATGCCACGCTACTGCGCAGCAGAGCGCTCTGCTCCG 1385
1731 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 1750
1386 TACCAGTACTTTGTTGTGACCCCATGGCTGAGTACACAGTCCGCCAGTATATCTTCGCT 1445
1751 TyrGlnTyrPheValValAspProMetAlaGluLysAsnMetProGlnTyrIleLeuArg 1770
1446 GAGTTCAGGTACGATGCCCGGATGGGAGTGGAGTCAAGCAATCCGCGAGTCCAGTTC 1505
1771 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
1506 ACAGCTGGCCAGACGAGGCGCTGCCAAGACAGCGGAGGATTCATTGACTTCATCGGG 1565
1791 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1810
1566 CAGGTGCATAGACAGAGGAGCAGTTGGACAGATGGGCTATCAGGTCAGTCCAGT 1625
1811 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1830
1626 GCTGCGTGGCGCCAGCCGCGGTGTTCATCTCTGAGCATCGTCCCTGGAGCGCATGCGC 1685

1831 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1850
1686 TATGAGGCGCTGTCGACATGTTTCACACCGTACAGACCGTGGTACACAGCGTCCCTGCC 1745
1851 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1870
1746 ATGCTGTCAGACAGAGGACCGATATCAGCTGTCTACCGTGGCCCTGGAGTACCTCGGC 1805
1871 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 1890
1806 ACCTTTCACCTATGCAACG 1826
1891 SerPheAspHisTyrAlaThr 1897
RESULT 10
AAU14143
ID AAU14143 standard; protein; 1907 AA.
XX AAU14143;
AC AAU14143;
DT 24-OCT-2001 (first entry)
XX Human novel protein #14.
DE Human; novel protein; Antianemic; osteopathic; antiinflammatory;
XX immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antisthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX Homo sapiens.
OS WO200155437-A2.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-US002623.
XX 25-JAN-2000; 2000US-00491404.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Dermanac RT;
XX WPI; 2001-451939/48.
XX N-PSDB; AAS22448.
XX Isolated polypeptides useful for treating anti-inflammatory diseases,
XX nervous system disorders, and for regenerating bone and cartilage.
XX Example 4; Page 533-537; 894pp; English.
XX The invention relates to polynucleotides encoding novel human proteins or
XX their active domains. The polypeptides, polynucleotides and antibodies
XX raised against the polypeptides are used in a method of treatment of a
XX mammal and prevention of disorders caused by the aberrant protein
XX expression or activity. The polypeptides can be used as molecular weight
XX markers, food supplements, and in antibody production. The polypeptides
XX are used to identify compounds which bind to the polypeptides.
XX Polynucleotides of the invention are used as probes and primers, for
XX sequencing, for chromosome or gene mapping, in the production of
XX recombinant proteins, and in generating anti-sense DNA or RNA and in gene
XX therapy. Polypeptides of the invention can be used to target drugs to a
XX tumour, in assays to determine biological activity, to raise
XX antibodies/elicit an immune response, to determine quantitative protein
XX levels, as tissue markers, and to isolate receptors or ligands.
XX Polypeptides of the invention may also be useful in treating platelet
XX disorders, stem cell disorders, regenerating bone, cartilage, tendon,
XX ligament and/or nerve tissue, wound healing, treating burns, promoting
XX the proliferation, differentiation and survival of stem cells, as a
XX contraceptive, treating osteoporosis and osteoarthritis, anaemia,

CC Alzheimer's, Parkinson's and Huntington's diseases, amyloidotic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
 CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
 CC diseases, nervous system disorders, and infection. The present sequence
 CC represents a protein of the invention
 XX
 SQ Sequence 1907 AA;

Alignment Scores:
 Pred. No.: 0 Length: 1907
 Score: 607.00 Matches: 607
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 53.34% Indels: 0
 DB: 4 Gaps: 0

US-09-719-272-1 (1-3467) x AAU14143 (1-1907)

QY 6 GGACTGAAGGACTCCTTGTGCGCCCACTCTCTGACCTGTGGAGATGCGGAGCTCAAC 65
 Db 1301 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgArgLeuAsn 1320

QY 66 TACGAGACCCAGGATGCGGAGACACACCCCACTCCCATCAGGACCTGCGGAGCAAC 125
 Db 1321 TyrGlnThrProGlyMetArgAspHisProProlIleThrAspLeuAlaAspAsn 1340

QY 126 ATCGAGCGCTCAAGCCCAACGATCGCTCAAGTTCTCCAGGAGTATGATCCTCATCGAC 185
 Db 1341 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 1360

QY 186 CTGACAGACGATTCACGTGGAGATTCMAACCTGGAGGTGACACAGCCCAAGACCGC 245
 Db 1361 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProGlyAsnArg 1380

QY 246 TATGGCAATGTCATCGCTTACGACCACTCTCGAGTCATCTTACCTCATCGATGGCGTC 305
 Db 1381 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1400

QY 306 CCGGGAGTGACTATCATATCCCACTACATCGATGCTACCGGACGACAGCAATGCCTAC 365
 Db 1401 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1420

QY 366 ATCGCCACGACGGCCCTGCGGAGACCACTGCGGCGATTTCTGGAGAAATGGTGGGAA 425
 Db 1421 IleAlaThrGlnGlyProLeuProGlnThrMetGlyAspPheTrpArgMetValTrpGlu 1440

QY 426 CAGCGCACGCGCCACTGTGTCTATGATGACACGCGTGGAGAGATCCCGGTTAAATGT 485
 Db 1441 GlnArgThrAlaThrValValMetMetThrArgLeuGluGluLysSerArgValLysCys 1460

QY 486 GATCAGTACTGCGCCGCGCGTGGCCAGACCTGTGGCTTATTTCAGTGACCTGTGTG 545
 Db 1461 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 1480

QY 546 GACACAGTGGAGCTGCCCATACACTGTGCGACCTTCGCACTCCCAAGAGTGGCTCC 605
 Db 1481 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 1500

QY 606 AGTGAGACGCTGAGCTGCTGAGTTTCAGTTTCATGGCTGGCCGACCATGGAGTTCCT 665
 Db 1501 SerGluLysArgGlnLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1520

QY 666 GAGTACCCCACTCCCATCTGCGCTTCTTACGACGGGTCAAGGCTCGAACCCCTAGAC 725
 Db 1521 GluTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 1540

QY 726 GCAGGCGCCATGTGTGTGACTGACGCGGGGGGTGGCGGCGGCTGCTTCATCTCG 785
 Db 1541 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1560

QY 786 ATTGATGCCATGTGGAGCGGATGAAGACGAGACGCGTGGACATCTATGCCACCGTG 845

RESULT 11
 AAB56372
 ID AAB56372 standard; protein; 442 AA.

Db 1561 IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal 1580
 QY 846 ACTTCATGCGCATCACAGAGAACTACATGCTGACAGCGAGGACCACTGCTGTTCATC 905
 Db 1581 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 1600
 QY 906 CATGAGGCGCTCTCGAGGCTGCCACGTGCGGCGCACACAGAGGTGCTGCCGCGCACTG 965
 Db 1601 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 1620

QY 966 TATGCCCATCCAGAGCTGGCCCAAGTCTCCAGGGGAGAGTGTACGCCCATGAG 1025
 Db 1621 TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu 1640

QY 1026 CTCGAGTTCAAGTTCTGCTGCCAGCTCCAAAGGCCCAACAGTCCCGCTTCATCAGCGCCAAC 1085
 Db 1641 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1660

QY 1086 CTGCCCTGCAACAAGTTCAGAAACCGGTGGTGAACATCATGCCCTCAAGATTGACCCGT 1145
 Db 1661 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1680

QY 1146 GTGTGTCTGCAGCCCATCCGTCTGTGGAGGCTCTGACTACATCAATGCCAGCTTCCTG 1205
 Db 1681 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 1700

QY 1206 GATGTTATAGACAGCAGAGGCTTACATAGCTACACAGGGGCTCTGCGAGAGACACC 1265
 Db 1701 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 1720

QY 1266 GAGGACTTCTGCGCATGCTATGGGAGCACAATTCACCATCATCGTCATGTCGACCAAG 1325
 Db 1721 GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLys 1740

QY 1326 CTTCGGGAGATGGCAGGAGGAATGCCACCACTACTGCCAGCAGACGCGTCTCTCGC 1385
 Db 1741 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 1760

QY 1386 TACCACTATTGTGTTTGCACCCGATGCTGAGTACAACATGCCCCAGTATCTCTCGCT 1445
 Db 1761 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 1780

QY 1446 GAGTTCAGGTACCGATCCCGGATGGGCGAGTCAAGACAAATCCGCGAGTCCAGTTC 1505
 Db 1781 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1800

QY 1506 ACAGACTGCGCAGCAGCGCGTGGCCCAAGACACAGCGAGGAGTTCATTGACTTCATCGG 1565
 Db 1801 ThrAspTrpProGlnGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1820

QY 1566 CAGGTGCATAAGACCAAGAGCAGATTGTGACAGGATGGGCTTATCACGGTGCAGTCCAGT 1625
 Db 1821 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1840

QY 1626 GCTGGGTGGCGCGCACCGGGTGTTCATCCTCTGAGCATCTCTGAGGCGCATCGCC 1685
 Db 1841 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1860

QY 1686 TATGAGGCGCTGCTGCACATGTTTCAGACCGTGAAGACCTCGGTACACAGCGTCTCGCC 1745
 Db 1861 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1880

QY 1746 ATGGTGCAGACAGAGGACCAATATCAGCTGCTACCGTGGCGGCTGGAGTACCTCGCGC 1805
 Db 1881 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 1900

QY 1806 AGCTTTGACCACCTATGCCACG 1826
 Db 1901 SerPheAspHisTyrAlaThr 1907

CX AAB56372;
 AC 13-MAR-2001 (first entry)
 CX Human prostate cancer antigen protein sequence SEQ ID NO:950.
 DE
 CX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 CX neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 CX vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
 CX antibacterial; gene therapy; neural; immune; reproductive; renal;
 CX gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 CX wound; infectious disease.
 CX Homo sapiens.
 XS
 CX WO200055174-A1.
 PN 21-SEP-2000.
 CX 08-MAR-2000; 2000WO-US005988.
 CX 12-MAR-1999; 99US-0124270P.
 CX (HUMA-) HUMAN GENOME SCI INC.
 CX (ROSE/) ROSEN C A.
 CX Rosen CA, Ruben SM;
 CX WPI; 2000-587513/55.
 CX N-PSDB; AAF15575.
 CX
 CX Prostate cancer associated gene sequences, referred to as prostate cancer
 CX antigens, useful for treatment, prevention, and diagnosis of disorders
 CX such as prostate cancer.
 CX Claim 11; Page 1389-1390; 2338pp; English.
 CX
 CX AAF15566 to AAF16505 encode the human prostate cancer associated
 CX proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CX The prostate cancer antigens can have neuroprotective, cytostatic,
 CX cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
 CX nephrotropic, antiinfective, gynaecological and antibacterial activities,
 CX and can be used in gene therapy. The prostate cancer antigen
 CX polynucleotides may be used for detection of prostate cancer, chromosome
 CX identification, as chromosome markers, and for numerous other diagnostic
 CX or research purposes. The prostate cancer antigens may be used to treat
 CX disorders such as neural, immune, muscular, reproductive,
 CX gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CX disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CX AAB57303 represent sequences used in the exemplification of the present
 CX invention
 CX
 CX Sequence 442 AA;
 SQ
 Alignment Scores:
 Pred. No.: 0 Length: 442
 Score: 442.00 Matches: 442
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 38.84% Indels: 0
 DB: 3 Gaps: 0
 US-09-719-272-1 (1-3467) x AAB56372 (1-442)
 QY 501 GCCGTGGCAGCAGACCTGGCCCTTATTCAGGTGACCTGTTGGACACAGTGGAGCTG 560
 Db 1 AlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrValGluLeu 20
 QY 561 GCACATACACTGTCGACCTTCACCTCCACAGAGTGGCTCCAGTGAAGACGCTGAG 620
 Db 21 AlaThrTyThrValArgThrPheAlaLeuHisSerGlySerGlySerGlyArgGlu 40

QY 621 CTGGCTCAGTTTCAGTTTCATGGCTGGCCAGACCATGGAGTTCCTGAGTACCAACTCCC 680
 Db 41 LeuArgGlnPheGlnPheMetAlaIleProAspHisGlyValProGluTyProThrPro 60
 QY 681 ATCTGGCCCTTCCTACACCGGCTCAGGCTGCAACCCCTAGACGAGGCGCCATGGTG 740
 Db 61 IleLeuAlaPheLeuArgValValAlaCysAsnProLeuAspAlaGlyProMetVal 80
 QY 741 GTGCACCTGCAGCGGGGGGGCCGACCGGCTGCTTCATCGTATGATGATGATGATGATG 800
 Db 81 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeu 100
 QY 801 GAGCGGTGAAGCAGACGAGACCGGTGACATCATATGCGCACGTCGACCTGCGATCA 860
 Db 101 GluArgMetLysHisGlyThrValAspIleTyGlyHisValThrCysMetArgSer 120
 QY 861 CAGAGGAACCTACATGGTGCAGACGGAGGACAGTACGTGTTTCATCCATGAGGGCTGCTG 920
 Db 121 GlnArgAsnTyMetValGlnThrGluAspGlnTyValPheIleHisGluAlaLeuLeu 140
 QY 921 GAGGCTGCCACGTGCGGCCACACAGAGTGCCTCCCGCAACCTGTATGCCCATCCAG 980
 Db 141 GluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeuTyAlaHisIleGln 160
 QY 981 AAGCTGGGCCAAGTGCCTCCAGGGGAGAGTGTGACCGCCATGGAGCTCGAGTCAAGTTG 1040
 Db 161 LysLeuGlyGlnValProProGlyLysValThrAlaMetGluLeuGluPheLysLeu 180
 QY 1041 CTGGCCAGCTCCAGGCCCCACACGCTCCCGCTTCATCAGCGCCAACTGCTCCCTGCAACAAG 1100
 Db 181 LeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLys 200
 QY 1101 TTCAGAACCCGGCTGGTGAACATCATGCCCTACGATTCAGATTCACCGTGTGTCTCCAGCCC 1160
 Db 201 PheLysAsnArgLeuValAsnIleMetProTyGluLeuThrArgValCysLeuGlnPro 220
 QY 1161 ATCCGTGTGTGGAGGCTCTGACTACATCATGCTCAGCTTCCTGGATGGTATTAGACAG 1220
 Db 221 IleArgGlyValGluGlySerAspTyIleAsnAlaSerPheLeuAspGlyTyArgGln 240
 QY 1221 CAGAGGCTCATAGCTACAGGCTTCAGGGGCTCTGGCAGAGACACCGAGACTTCTGGGCGC 1280
 Db 241 GlnLysAlaTyIleAlaThrGlnGlyProLeuAlaGluSerThrGluAspPheTyArg 260
 QY 1281 ATGCTATGGAGCAAAATCCACCATCATCTGCTGCTGACCAAGCTTCGGGAGATGGGC 1340
 Db 261 MetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLysLeuArgGluMetGly 280
 QY 1341 AGGGAGAAATGCCACCTACTGCGCCAGACGAGCGCTCTGCTCGCTACAGTACTTTGTT 1400
 Db 281 ArgGluLysCysHisGlnTyTrpProAlaGluArgSerAlaArgTyGlnTyPheVal 300
 QY 1401 GTTGACCGATGGCTGAGTACACATGCCCGCCAGTATATCCTCGGTGAGTTCAGGTCAAG 1460
 Db 301 ValAspProMetAlaGluTyAsnMetProGlnTyIleLeuArgGluPheLysValThr 320
 QY 1461 GATGCCCGGGATGGGCACTCAAGGACAAATCCGGCAGTTCAGTTCACAGACTGGCCAGAG 1520
 Db 321 AspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGlu 340
 QY 1521 CAGGGGTGCCCAACACAGAGGCGAGGATTCATTGACTTCATCGGCGAGTGCATTAAGACC 1580
 Db 341 GlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGlnValHisLysThr 360
 QY 1581 AAGGAGCAGTTCGGACAGGATGGGCTATCAGCGTGCATCTGCGTGCAGTGTGGCGGCGCC 1640
 Db 361 LysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArg 380
 QY 1641 ACCGGGTGTTTCACTCTGAGCATCGTCTGGAGCGCATGCGCTATGAGGCGGTGTC 1700
 Db 381 ThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArgTyGluGlyValVal 400
 QY 1701 GACATGTTTTCAGACCGTGAAGACCCCTGGGTACACAGCGCTCTGCTGCCATGCTGTCAGACAG 1760

Db 401 AspMetPheGlnThrValIysThrLeuArgThrGlnArgProAlaMetValGlnThrGlu 420
QY 1761 GACCAAGTATCAGCTGTGCTACCGTGGCCCTGGAGTACCTCGGACGCTTTGACCACTAT 1820
Db 421 AspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGlySerPheAspHisTyr 440
QY 1821 GCAACG 1826
Db 441 AlaThr 442
RESULT 12
ABM78984
ID ABM78984 standard; protein; 296 AA.
XX AC ABM78984;
XX 15-JAN-2004 (first entry)
XX Human leukocyte common antigen related protein.
XX DE Human; leukocyte common antigen related protein; LAR;
XX KW protein tyrosine phosphatase; enzyme.
XX OS Homo sapiens.
XX WO2003073987-A2.
XX PD 12-SEP-2003.
XX 26-FEB-2003; 2003WO-US005950.
XX PF 01-MAR-2002; 2002US-0361475P.
XX PR 25-FEB-2003; 2003US-00374539.
XX PA (SUNE-) SUNESIS PHARM INC.
XX PI Barr K, Fahr B, Hansen S, Wiesmann C;
XX WPI; 2003-756750/71.
XX New 3,5 dibromo-4-hydroxybenzene carbonyl benzofuran derivatives
PT inhibiting protein tyrosine phosphatase and T-cell protein tyrosine
PT phosphatase are useful to treat e.g. type 2 diabetes, inflammation and
PT immune system disorders.
XX Disclosure; Fig 7; 58pp; English.
XX The present sequence is the protein sequence of human protein tyrosine
CC phosphatase leukocyte common antigen related protein (LAR). The invention
CC provides novel 3,5-dibromo-4-hydroxybenzene carbonyl benzofuran
CC derivatives that modulate the activity of human protein tyrosine
CC phosphatase 1B (PTP-1B, see ABM78982) by binding to a novel binding site,
CC termed the exosite, that is distal to the PTP-1B active site. These
CC compounds do not inhibit LAR, in which the exosite-forming residues of
CC PTP-1B are generally not conserved. The compounds are useful for treating
CC diabetes and/or its associated complications such as insulin resistance
CC and obesity
XX SQ Sequence 296 AA;
Alignment Scores:
Pred. No.: 4,98e-274 Length: 296
Score: 296.00 Matches: 296
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.01% Indels: 0
Gaps: 0
DB:
US-09-719-272-1 (1-3467) x ABM78984 (1-296)
QY 102 CCATACCGACCTGGCGGACACATCGAGCGCTCAAGCCAAACGATGGCTCAAGTTC 161

Db 1 ProIleThrAspLeuAlaAspAsnIleGluArgLeuLysAlaAsnAspGlyLeuLysPhe 20
QY 162 TCCAGGAGTATGAGTCCATCGACCTCGACAGACGAGTTACGTTGGGAGAAATCAAAACCTG 221
Db 21 SerGlnGluTyrGluSerIleAspProGlyGlnGlnPheThrTrpGluAsnSerAsnLeu 40
QY 222 GAGGTGAACACAGCCCAAGAACCGCTATCGAATGTGCATCGCTACGACCACTCTCGAGTC 281
Db 41 GluValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHisSerArgVal 60
QY 282 ATCTTACCTCTATCGATGGCGTCCCGGGAGTGAATCATCAATGCCAATCATCATCAT 341
Db 61 IleLeuThrSerIleAspGlyValProGlySerAspTyrIleAsnAlaAsnTyrIleAsp 80
QY 342 GGCTACCGCAAGCAGAAATCGCTACATCGCAGCGAGGCCCTCCCGGACGACCAATGGGC 401
Db 81 GlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGlyProLeuProGluThrMetGly 100
QY 402 GATTTCTGAGAAATGTTGGGAAACAGCGCAGCGGCACTGTGGTTCATGATGACACGGCTG 461
Db 101 AspPheTrpArgMetValTrpGluGlnArgThrAlaThrValValMetMetThrArgLeu 120
QY 462 GAGGAGAAGTCCCGGTAAATGTGATCAGTACTGCGCAGCGCGCTGGCACCAGACCTGT 521
Db 121 GluGluLysSerArgValLysCysAspGlnTyrTrpProAlaArgGlyThrGluThrCys 140
QY 522 GGCTTTATTCAGTGACCTGTGGACACAGTGGAGTGGCCACATACACTGTGTGGCCACC 581
Db 141 GlyLeuIleGlnValThrLeuLeuAspThrValGluLeuAlaThrTyrThrValArgThr 160
QY 582 TTCGCATCCACAAGAGTGGCTCCAGTGAGAGCGGTGAGCTCGCTCAGTTTCAGTTTCATG 641
Db 161 PheAlaLeuHisLysSerGlySerGluLysArgGluLeuArgGlnPheGlnPheMet 180
QY 642 GCCTGCCACAGACCATGAGTCTCTGAGTACCACCACTCCCATCTGGCTTCTCTACAGCG 701
Db 181 AlaTrpProAspHisGlyValProGluTyrProThrProIleLeuAlaPheLeuArgArg 200
QY 702 GTCAGGCGCTGCAACCCCTAGACGCGAGGCCCATGCTGGTGCCTGACGCGCGGCGCTG 761
Db 201 ValLysAlaCysAsnProLeuAspAlaGlyProMetValValHisCysSerAlaGlyVal 220
QY 762 GGCCGACCGCGCTGCTTCTATCGTGTATGATGATGATGATGATGATGATGATGATGATG 821
Db 221 GlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluArgMetLysHisGluLys 240
QY 822 ACGGTGGACATCTATGCGCACGCTGACCTGCATCGCATCACAGGAGGAACATCATGTCAG 881
Db 241 ThrValAspIleTyrGlyHisValThrCysMetArgSerGlnArgAsnTyrMetValGln 260
QY 882 ACGGAGGACGAGTACGTGTTCATCCATGAGGCGCTGCTGGAGGCTGCCACGTCGCGCCAC 941
Db 261 ThrGluAspGlnTyrValPheIleHisGluAlaLeuLeuGluAlaAlaThrCysGlyHis 280
QY 942 ACGAGGTGCTCCCGCAACCTGTATGCCCATCCATCCAGAACTGGGC 989
Db 281 ThrGluValProAlaArgAsnLeuTyrAlaHisIleGlnLysLeuGly 296
RESULT 13
ABM78268
ID ABM78268 standard; protein; 306 AA.
XX AC ABM78268;
XX 19-DEC-2001 (first entry)
XX Human DCA-D1.
XX KW PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
XX dephosphorylation; phosphotyrosine; human; PTP1B; mouse; fruit fly;
XX yeast.
XX OS Homo sapiens.

XX FN WO200161031-A2.
 XX PD 23-AUG-2001.
 XX PF 13-FEB-2001; 2001WO-US005180.
 XX PR 14-FEB-2000; 2000US-0181769P.
 XX PA (CEPT-) CEPTYR INC.
 XX PI Flint AJ, Cool DE;
 XX PK WPI; 2001-570570/64.
 XX PT Screening assays to identify agents that alter protein tyrosine
 PT phosphatase (PTP) binding to, and PTP-mediated catalytic
 PT dephosphorylation of phosphotyrosine peptide substrates.
 XX XX Disclosure; Fig 1; 79pp; English.
 XX XX The invention relates to identifying agents which alter the interaction
 XX between a protein tyrosine phosphatase (PTP) and a tyrosine
 XX phosphorylated polypeptide using fluorescence energy signals. The methods
 XX are useful for performing screening assay to identify agents that alter
 XX PTP binding to and PTP-mediated catalytic dephosphorylation of
 XX phosphotyrosine peptide substrates. The present sequence is that of a
 XX catalytic domain of a PTP for comparison with human PTP1B (AAG78262)
 XX XX Sequence 306 AA;
 XX
 Alignment Scores:
 Pred. No.: 5.75e-184 Length: 306
 Score: 202.00 Matches: 250
 Percent Similarity: 97.86% Conservative: 0
 Best Local Similarity: 97.66% Mismatches: 0
 Query Match: 17.75% Indels: 6
 DB: 4 Gaps: 0
 US-09-719-272-1 (1-3467) x AAG78268 (1-306)
 QY 195 CAGTTCAGTCGGAGAAATTCACCTGGAGTGAGAACAGCGCAAGACCCCTATGCAAT 254
 DB 1 GlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArgTyrAlaAsn 20
 QY 255 GTCATCGCTACGACCTCCGAGTCATCTTACCTCTATCGATGCGTCCCGGGAGT 314
 DB 21 ValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyValProGlySer 40
 QY 315 GACTACATCAATGCCAACTACATCGATGGCTACCGCAAGCAGAGATGCTACATCGCCACG 374
 DB 41 AspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThr 60
 QY 375 CAGGCGCCCTCGCCGACCATCGGGGATTTCTGGAGATGGTGTGGAAACAGCGCAGC 434
 DB 61 GlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGluGlnArgThr 80
 QY 435 GCCACTGTGTGTCATGACACGCGTCGAGGAGAGTCCCGGGTAAATGTGATCAGTAC 494
 DB 81 AlaThrValValMetMetThrArgLeuGluGluLysSerArgValLysCysAspGlnTyr 100
 QY 495 TGGCAGCCCTGGCCACCGACCTGGCCCTTATTCAGTGTGACCCCTGGGACACAGTG 554
 DB 101 TrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrVal 120
 QY 555 GAGCTGGCCACATACATCTGTGCGCACCTTCGCACTCCACAGATGGCTCCAGTGAGAAG 614
 DB 121 GluLeuAlaThrTyrThrVal-----PheAlaLeuHisLysSerGlySerSerGluLys 138
 QY 615 CGTGAGTCGCTCAGTTTCAGTTTCAGTTTCAGTTTCAGTTTCAGTTTCAGTTTCAGTTCC 674
 DB 139 ArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrPro 158

QY 675 ACTCCATCTGGCCTTCCTTACGACGGGTCAAGCGCTGCAACCCCTAGACGCGAGGCCCC 734
 DB 159 ThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAspAlaGlyPro 178
 QY 735 ATGTGGTGCTACTGCAGCGCGGGCTGGCGCACCGCTGCTTTCATCGTATTGATGCC 794
 DB 179 MetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAla 198
 QY 795 ATGTTGGAGCGGATGAACACGACGAGACGCGTGACATCTATGGCCACGTGACCTGCATG 854
 DB 199 MetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisValThrCysMet 218
 QY 855 CGATCAGAGAGAACTACATGTCGACGACGAGGACGACGACGAGTTCATCCATGAGCG 914
 DB 219 ArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGluAla 238
 QY 915 CTGCTGGAGGCTGCCACGTGCGGCGCACACAGAGTG 950
 DB 239 LeuLeuGluAlaAlaThrCysGlyHisThrGluVal 250
 RESULT 14
 AAG78287
 ID AAG78287 standard; protein; 294 AA.
 XX AC AAG78287;
 XX DT 19-DEC-2001 (first entry)
 XX DE Human BCA-D2.
 XX PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
 KW dephosphorylation; phosphotyrosine; human; PTP1B; mouse; fruit fly;
 KW yeast.
 OS Homo sapiens.
 FN WO200161031-A2.
 PD 23-AUG-2001.
 PF 13-FEB-2001; 2001WO-US005180.
 PR 14-FEB-2000; 2000US-0181769P.
 XX (CEPT-) CEPTYR INC.
 XX Flint AJ, Cool DE;
 XX WPI; 2001-570570/64.
 XX Screening assays to identify agents that alter protein tyrosine
 PT phosphatase (PTP) binding to, and PTP-mediated catalytic
 PT dephosphorylation of phosphotyrosine peptide substrates.
 XX XX Disclosure; Fig 1; 79pp; English.
 XX The invention relates to identifying agents which alter the interaction
 CC between a protein tyrosine phosphatase (PTP) and a tyrosine
 CC phosphorylated polypeptide using fluorescence energy signals. The methods
 CC are useful for performing screening assay to identify agents that alter
 CC PTP binding to and PTP-mediated catalytic dephosphorylation of
 CC phosphotyrosine peptide substrates. The present sequence is that of a
 CC catalytic domain of a PTP for comparison with human PTP1B (AAG78262)
 XX XX Sequence 294 AA;
 SQ
 Alignment Scores:
 Pred. No.: 3.57e-179 Length: 294
 Score: 197.00 Matches: 245
 Percent Similarity: 97.61% Conservative: 0
 Best Local Similarity: 97.61% Mismatches: 0
 Query Match: 17.31% Indels: 6
 DB: 4 Gaps: 0

US-09-719-272-1 (1-3467) x AAG78287 (1-294)

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Db 21 IleMetProTyrGluLeuThrArgValCysLeuGlnProIleArgGlyValGluGlySer 40
QY 1182 GACTACATCAATGCCAGCTTCTGTGATGTTATAGACAGGAGGCTCATAGCTACA 1241
Db 41 AspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnLysAlaTyrIleAlaThr 60
QY 1242 CAGGGCGCTCTGGCAGAGACCCAGGACTCTGGCGCATCTATGGGACACAAATTC 1301
Db 61 GlnGlyProLeuAlaGlnSerThrGluAspPheTyrArgMetLeuTyrGluHisAsnSer 80
QY 1302 ACCATCATGTCATCTGACCAAGCTTCGGAGATGGCAGGAGAAATGCCACAGTAC 1361
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QY 1362 TGGCCAGCAGAGCGCTCTGCTGCTGCTACCACTACTTGTGTGTGACCCGATGGCTGAGTAC 1421
Db 101 TrpProAlaGluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGlnTyr 120
QY 1422 AACATGCCCGCATATATCTCGTGTGAGTTCAGGTCACGGATGCCGGATGGCATCA 1481
Db 121 AsnMetProGlnTyrIleLeu-----PheLysValThrAspAlaArgAspGlyGlnSer 138
QY 1482 AGGACAATCCGGCAGTTCAGTTCCAGACTGCACACTGGCCAGAGCAGGCGTCCCAAGACAGGC 1541
Db 139 ArgThrIleArgGlnPheGlnPheThrAspTyrProGluGlnGlyValProLysThrGly 158
QY 1542 GAGGATTCATTGACTTCATCCGGCAGGTGCATAGACCAAGGAGCAGTTTGGACAGAT 1601
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QY 1602 GGGCTATCAGCGTCACTGCACTGCTGCGTGGCGCCGCGCGGTTCATCACTCTG 1661
Db 179 GlyProIleThrValHisCysSerAlaGlyValGlyArgThrGlyValPheIleThrLeu 198
QY 1662 AGCATCGTCTGGAGCGCATGCGCTATGAGGCGTGTGCGACATGTTTCAGACCGTGAAG 1721
Db 199 SerIleValLeuGluArgMetArgTyrGluGlyValValAspMetPheGlnThrValLys 218
QY 1722 ACCCTGCTACACAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1781
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RESULT 15
AAB59370
ID AAB59370 standard; protein; 250 AA.

XX AAB59370;

XX AC AAB59370;

XX XX 21-MAR-2001 (first entry)

XX DE Human protein tyrosine phosphatase #6.

XX KW Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;

XX KW substrate trapping.

XX XX Homo sapiens.

XX OS Homo sapiens.

XX PN WO200075339-A1.

XX XX 14-DEC-2000.

XX 24-MAY-2000; 2000WO-US014211.
XX PF
XX 03-JUN-1999; 98US-0137313P.
XX PR 16-JUN-1999; 99US-00334575.
XX PA (COLD-) COLD SPRING HARBOR LAB.
XX Tonks NK, Zhang S;
XX WPI; 2001-080598/09.

XX New substrate trapping mutant protein tyrosine phosphatases (PTP) in
PT which the wild type PTP catalytic domain invariant apparatus is replaced
PT with an unphosphorylated amino acid, useful in gene therapy.

XX Disclosure; Fig 1; 109pp; English.

XX The present invention provides substrate trapping mutant protein tyrosine
CC phosphatases (PTP). They can be used to reduce the activity of tyrosine
CC phosphorylated proteins and to screen for modulators capable of altering
CC the binding of protein tyrosine phosphatases to their substrate. These
CC may be used in disease diagnosis and treatment

XX Sequence 250 AA;

Alignment Scores:
Pred. No.: 1,648-125 Length: 250
Score: 141.00 Matches: 189
Percent Similarity: 96.92% Conservative: 0
Best Local Similarity: 96.92% Mismatches: 0
Query Match: 12.39% Indels: 6
DB: 4 Gaps: 0

US-09-719-272-1 (1-3467) x AAB59370 (1-250)

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QY 498 CCAGCCCGTGGCAGCAGACCTGTGCGCTTATTCAGGTGACCTCTTGGACACAGTGAG 557
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QY 558 CTGGCCACATACACTGTGGCGACCTTGGCCTCCACACAGAGTGGCTCCAGTGAGAGCGT 617
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QY 618 GAGCTCGCTCAGTTTCAGTTTCATGCGCTGGCCAGACCATGGAGTTCTCTGATCCCAACT 677
Db 140 GluLeuArgGlnPheGlnPheMetAlaTyrProAspHisGlyValProGluTyrProThr 159
QY 678 CCCATCTCGCTTCTTACAGCGGTCAAGGCTGCAACCCCTAGACGCGAGCGCCATG 737
Db 160 ProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAspAlaGlyProMet 179
QY 738 GTGCTGCTGCTGAGCGCGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797
Db 180 ValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMet 199
QY 798 TTGAGCGGATGAGCAGAGAGCGGTGGACATCTATGGCCAGTGCATCTGCTGCTGCTG 857
Db 200 LeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisValThrCysMetArg 219
QY 858 TCACAGAGGAACCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 917
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QY 918 CTGGAGGCTGCCACGTGGCGGCCACACAGAGGTG 950
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2b 240 LeuGluAlaAlaThrCysGlyHisThrGluVal 250

Search completed: March 9, 2004, 09:03:18
Job time : 205 secs

GenCore version 5.1.1.6
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M nucleic - protein search, using frame_plus_n2p model

Run on: March 9, 2004, 09:03:24 ; Search time 115 Seconds
(without alignments)

12731.623 Million cell updates/sec

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 809742 seqs, 211153259 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1535912

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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MAXLEN=200000000 -USERS=US0919272 @CEN 1 1 23 @runat_09032004_085231_7520
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Database : Published Applications AA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description

ALIGNMENTS

RESULT 1

US-10-291-265-722
Sequence 722, Application US/10291265
Publication No. US20030232054A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al
TITLE OF INVENTION: No. US20030232054A1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10291265
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 722
LENGTH: 647
TYPE: PRT

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442	38.8	442	9	US-09-925-300-950	Sequence 950, App
296	26.0	296	14	US-10-374-539-3	Sequence 3, Appl
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289	25.4	289	14	US-10-314-232-13	Sequence 13, Appl
202	17.8	306	9	US-09-788-626-8	Sequence 8, Appl
197	17.3	294	9	US-09-788-626-27	Sequence 27, Appl
5	5.2	1502	10	US-09-808-602-54	Sequence 54, Appl
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12	5.2	1948	10	US-09-800-198-45	Sequence 45, Appl
55	4.9	57	14	US-10-029-386-29636	Sequence 29636, A
40	3.5	1425	15	US-10-258-666-12	Sequence 12, Appl
30	2.6	162	15	US-10-334-143-151	Sequence 151, App
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19	1.4	176	14	US-10-314-233-9	Sequence 9, Appl
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21	1.2	322	14	US-10-314-232-11	Sequence 11, Appl
22	1.2	354	10	US-09-095-478-6	Sequence 6, Appl
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24	1.2	401	14	US-10-314-232-15	Sequence 15, Appl
25	1.2	412	10	US-09-095-478-3	Sequence 3, Appl
26	1.2	426	10	US-09-095-478-1	Sequence 1, Appl
27	1.2	463	10	US-09-095-478-2	Sequence 2, Appl
28	1.2	898	14	US-10-314-232-22	Sequence 22, Appl
29	1.2	2291	10	US-09-822-871-2	Sequence 2, Appl
30	1.2	2301	10	US-09-822-871-4	Sequence 4, Appl
31	1.1	20	14	US-10-340-288-25	Sequence 25, Appl
32	1.1	33	15	US-10-052-648A-85	Sequence 85, Appl
33	1.1	98	15	US-10-074-978A-323	Sequence 323, App
34	1.1	248	9	US-09-848-294-10	Sequence 10, Appl
35	1.1	248	14	US-10-293-231-10	Sequence 10, Appl
36	1.1	264	14	US-10-245-539-6	Sequence 6, Appl
37	1.1	292	14	US-10-314-232-12	Sequence 12, Appl
38	1.1	309	9	US-09-788-626-11	Sequence 11, Appl
39	1.1	309	9	US-09-788-626-12	Sequence 12, Appl
40	1.1	310	9	US-09-788-626-10	Sequence 10, Appl
41	1.1	310	9	US-09-788-626-15	Sequence 15, Appl
42	1.1	313	9	US-09-788-626-7	Sequence 7, Appl
43	1.1	316	9	US-09-788-626-5	Sequence 5, Appl
44	1.1	316	9	US-09-788-626-26	Sequence 26, Appl
45	1.1	317	9	US-09-788-626-4	Sequence 4, Appl

ORGANISM: Homo sapiens
US-10-291-265-722

Alignment Scores:

Pred. No.: 0 Length: 647
Score: 607.00 Matches: 607
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.34% Indels: 0
DB: 15 Gaps: 0

US-09-719-272-1 (1-3467) x US-10-291-265-722 (1-647)

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DB 81 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 100
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RESULT 2

US-10-291-265-250
; Sequence 250, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US920030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)

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CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 250
LENGTH: 1907
TYPE: PRT
ORGANISM: Homo sapiens
10-291-265-250

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Score:	607.00	Matches:	607	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Nucly Match:	53.34%	Indels:	0	
IB:	15	Gaps:	0	
JS-09-719-272-1 (1-3467) x US-10-291-265-250 (1-1907)				
6	GGACTGAAGGACTCCTTGCTGGCCCACTCTCTGACCTCTGGAGATCGGAGGCTCAAC	65		
XY				
1301	GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgArgLeuAsn	1320		
YY				
66	TACCAGACCCAGGTATGCGAGACCAACCACCCATCCCATCCGACCTGGCGGACAAC	1325		
YY				
1321	TyrGlnThrProGlyMetArgAspHisProProlleThrAspLeuAlaAspAsn	1340		
YY				
126	ATCGAGCGCCTCAAGCAACGATGGCTCAAGTTCTCCAGGAGTATGAGTCATCGAC	1355		
YY				
1341	IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGlyArgSerIleAsp	1360		
YY				
186	CTGCGACAGCAGTTCACGTGGGAGAAATTCAAACCTGGAGGTGAACACGCCAAGAACCGC	245		
YY				
1361	ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg	1380		
YY				
246	TATGCGAATGTCATCGGCTACGACCACTCTCGAGTCATCTTACCTCTATCGATGGGCTC	305		
YY				
1381	TyrAlaAsnValIleAlaTyArgHisSerArgValIleLeuThrSerIleAspGlyVal	1400		
DB				
306	CCCGGAGTGACTACATCAATGCCAACTACATCGATGGCTACCGACGACGAAGTCCTTAC	365		
YY				
1401	ProGlySerAspTyrlleAsnAlaAsnTyrlleAspGlyTyArgLysGlnAsnAlaTy	1420		
YY				
366	ATCGCGCAGCAGGCGCCCTGCCCGACACCATGGCGGATTTCTGGAGAAATGCTGTGGAA	425		
YY				
1421	IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu	1440		
YY				
426	CAGCGCAGCGGCATCTGGTCATGATGACACGGCTCGAGGAGAGTCCCGGTTAAATGT	485		
YY				
1441	GlnArgThrAlaThrValValMetMetThrArgLeuGluGlySerArgValLysCys	1460		
DB				
486	GATCAGTACTGGCAGCCGCGGACCGACGACCTGTGGCTTATTTCAGGTGACCCGTGTG	545		
QY				
1461	AspGlnTyTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu	1480		
DB				
546	GACACAGTGGAGCTGGCCACATACACTGTGCGCACCTTCGCACTCCACAAGAGTGGCTCC	605		
QY				
1481	AspThrValGluLeuAlaThrTyThrValArgThrPheAlaLeuHisLysSerGlySer	1500		
DB				
606	AGTGAGAGCGTGAGCTCGCTCAGTTTCAGTTTCATGTGCTGGCCGACCATCGAGTCTCT	665		
QY				
1501	SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro	1520		
DB				
666	GAGTACCCAACTCCCATCTCGGCTTCTCTACGCGGGTCAAGGCTGCAACCCCTAGAC	725		
QY				

Db 1881 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 1900

2Y 1806 AGCTTTCACCATATGCAACG 1826

Db 1901 SerPheAspHisTyrAlaThr 1907

RESULT 3

US-09-925-300-950

Sequence 950, Application US/09925300

Patent No. US20020151681A1

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Steve Ruben

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05988

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 950

LENGTH: 442

TYPE: PRT

ORGANISM: Homo sapiens

US-09-925-300-950

Alignment Scores:

Pred. No.: 0 Length: 442

Score: 442.00 Matches: 442

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 38.84% Indels: 0

DB: 9 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-925-300-950 (1-442)

QY 501 GCCCTGGACCGACGCTGGCTTATTCAGTGGACCCCTGGACACAGTGGAGCTG 560

Db 1 AlaArgGlyThrGluThrCysGlyLeuGlnValThrLeuLeuAspThrValGluLeu 20

QY 561 GCACATACACTGTCCGACCTTCGACATCCACAGAGTGGCTCCAGTGAGAACGCTGAG 620

Db 21 AlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySerGlyLeuValGlu 40

QY 621 CTGCTCAGTTTCAGTTTCAGTGGCTGGCCAGACCATGAGTTCCTGAGTACCCCACTCCC 680

Db 41 LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrProThrPro 60

QY 681 ATCTCTGGCTTCTCTACGACGGGTCAAGGCTGCAACCCCTAGACGCGACGGCCCATGGTG 740

Db 61 IleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAspAlaGlyProMetVal 80

QY 741 GTGCACTGACGGCGGCTGGCCGCGACCGCTCTTCATCGTATGATGCGCATGGTG 800

Db 81 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeu 100

QY 801 GAGCGCATCAAGCACGAGAACGGTGGACATCTATGGCCAGCTGACCTGCATGCGATCA 860

Db 101 GluArgMetLysHisGluLysThrValAspIleTyrGlyHisValThrCysMetArgSer 120

QY 861 CAGAGAACTACATGTGTGACGAGGACCACTAGCTGTTCATCATGAGCGCTGCTG 920

Db 121 GlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGluAlaLeuLeu 140

QY 921 GAGGCTGCCACGTGGCCGACACAGAGGTGCTGCCGCCAACCTGTATGCCACATCCAG 980

Db 141 GluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeuTyrAlaHisIleGln 160

QY 981 AAGCTGGGCCAAGTGGCTCCAGGGGAGAGTGGACCGCCATGAGCTGAGTTCAGTTG 1040

Db 161 LysLeuGlyGlnValProProGlyGluSerValThrAlaMetGluLeuGluPheLysLeu 180

QY 1041 CTGGCCAGCTCCAGGCGCCACACGTCCTCCGCTTCATCAGCCCAACCTGCTGCAACAAG 1100

Db 181 LeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLys 200

QY 1101 TTCAGAACCGCTGTGAAACATCATGCTAGCAATTGACCCGTGTGTCTCTGCACGCC 1160

Db 201 PheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArgValCysLeuGlnPro 220

QY 1161 ATCCGTGTGTGGAGGCTCTGACTACATCAATGCCAGCTTCCTGGATGTTATAGACAG 1220

Db 221 IleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGln 240

QY 1221 CAGAAGGCTACATAGCTACACAGGGCTCTGGCAGAGGACCCGAGGACTTCTGCGCG 1280

Db 241 GlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThrGluAspPheTyrArg 260

QY 1281 ATGCTATGGAGACCAATTCCACCATCATGCTCATGTCCAGCAAGCTTCGGGAGATGGC 1340

Db 261 MetLeuTrpGluHisAsnSerThrIleValMetLeuThrLysLeuArgGluMetGly 280

QY 1341 AGGAGAAATGCCACCACTACTGCGCAGCAGAGCGCTCTGCTCCCTACCACTACTTGT 1400

Db 281 ArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArgTyrGlnTyrPheVal 300

QY 1401 GTTGACCCGATGGCTGAGTACAACATGCCAGCTATATCTCTCGTGGATTCAGGTCAAG 1460

Db 301 ValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArgGluPheLysValThr 320

QY 1461 GATGCCCGGATGGGCACTCAAGACATCCGCGAGTCCAGTTCACAGCTGGCCAGAG 1520

Db 321 AspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGlu 340

QY 1521 CAGGCGCTGCCCAACAGACAGCGGAGGATTCATTGACTTCATCGGCGCAGGTGCATAAGACC 1580

Db 341 GlnGlyValProLysThrGlyGlyPheIleAspPheIleGlyGlnValHisLysThr 360

QY 1581 AAGGAGCAAGTTGGACAGATGGGCTATCAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 1640

Db 361 LysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArg 380

QY 1641 ACCGGGTGTTTCATCTCAGTCTGAGCATCTCTGGAGCGCATGCTGATGAGGGGTGCTC 1700

Db 381 ThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArgTyrGluGlyValVal 400

QY 1701 GACATGTTTCAGACCGTGAAGACCTCGGTATCAGCGTCTCTGCTGCTGCTGCTGCTGCTG 1760

Db 401 AspMetPheGlnThrValLysThrLeuArgThrGlnArgProAlaMetValGlnThrGlu 420

QY 1761 GACCATATCAGTGTGTACCGTGTACCGTGTGAGTACCTCGGCGAGCTTTGACCACTAT 1820

Db 421 AspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGlySerPheAspHisTyr 440

QY 1821 GCAACG 1826

Db 441 AlaThr 442

RESULT 4

US-10-374-539-3

Sequence 3, Application US/10374539

Publication No. US20030195247A1

GENERAL INFORMATION:

APPLICANT: SUNESIS PHARMACEUTICALS, INC.

APPLICANT: BARR, Kenneth

APPLICANT: FARR, Bruce

APPLICANT: HANSEN, Stig

APPLICANT: McDOWELL, Robert

APPLICANT: WIESMAN, Chris

APPLICANT: ZHU, Jian

TITLE OF INVENTION: COMPOUNDS THAT MODULATE THE ACTIVITY OF

TITLE OF INVENTION: PTP-1B AND TC-PTP

FILE REFERENCE: 39750-0008

CURRENT APPLICATION NUMBER: US/10/374,539
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 60/361,475
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 296
TYPE: PRT
ORGANISM: Homo sapiens
US-10-374-539-3

Alignment Scores:
Seq. No.: 5,23e-260 Length: 296
Score: 296.00 Matches: 296
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.01% Indels: 0
Gaps: 14

US-09-719-272-1 (1-3467) x US-10-374-539-3 (1-296)

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102 CCATCAGGAGTATGAGTCCGAGCAACATCGAGCGCTCAAGCCAAAGCCAAAGCATGGCTCAAGTTC 161
1 ProlethrAspLeuAlaAspAsnIleGluArgLeuLysAlaAsnAspGlyLeuLysPhe 20
162 TCCAGGAGTATGAGTCCGAGCAACATCGAGCGCTCAAGCCAAAGCCAAAGCATGGCTCAAGTTC 221
21 SerGlnGluThrAspLeuAlaAspAsnIleGluArgLeuLysAlaAsnAspGlyLeuLysPhe 40
222 GAGGTGAACAAAGCCAAAGCCAAAGCCAAAGCCAAAGCCAAAGCCAAAGCCAAAGCCAAAGCCAA 281
41 GluValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHisSerArgVal 60
282 ATCTTACCTCTATCGATGGCTCCCGGAGTGCATCATCGCTCAAGCCAAAGCCAAAGCCAAAGCCAA 341
61 IleLeuThrSerIleAspGlyValProGlySerAspTyrIleAsnAlaAsnTyrIleAsp 80
342 GGTACCGCAGCAAGATGCTACATCGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 401
81 GlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGlyProLeuProGluThrMetGly 100
402 GATTCTCGAGTATGAGTCCGAGCAACATCGAGCGCTCAAGCCAAAGCCAAAGCCAAAGCCAAAGCC 461
101 AspPheTrpArgMetValTrpGluGlnArgThrAlaThrValValMetThrArgLeu 120
462 GAGGAGAAAGTCCCGGGTAAATGTGATCAGTACGTGGCCAGCCCGTGGCCAGCCAGCCAGCCAGCC 521
221 GlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluArgMetLysHisGluLys 240
822 ACGGTGACATCTATGGCCAGTGAACCTGATCGATCGATCGATCGATCGATCGATCGATCGATCGAT 881
241 ThrValAspIleTyrGlyHisValThrCysMetArgSerGlnArgAsnTyrMetValGln 260
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QY 882 ACGGAGGACGAGTATGAGTCCGAGCAACATCGAGCGCTCAAGCCAAAGCCAAAGCCAAAGCCAA 941
Db 261 ThrGluAspGlnTyrValPheIleHisGluAlaLeuLeuAlaAlaThrCysGlyHis 280
QY 942 ACGAGGTGCTGCTCCCGCAACCTGTATGCCACATCCAGAAAGCTGGGC 989
Db 281 ThrGluValProAlaArgAsnLeuTyrAlaHisIleGlnLysLeuGly 296
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RESULT 5

US-10-374-499-9
Sequence 9, Application US/10374499
Publication No. US20040005632A1
GENERAL INFORMATION:
APPLICANT: SUNESIS PHARMACEUTICALS, INC.
APPLICANT: ERLANSON, Daniel A.
APPLICANT: MCDOWELL, Robert S.
TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS THAT
TITLE OF INVENTION: MODULATE ENZYMACTIC ACTIVITY
FILE REFERENCE: 39750-0016
CURRENT APPLICATION NUMBER: US/10/374,499
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 60/377,034
PRIOR FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: US 10/121,216
PRIOR FILING DATE: 2002-04-10
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 296
TYPE: PRT
ORGANISM: Homo sapiens
US-10-374-499-9

Alignment Scores:
Seq. No.: 5,23e-260 Length: 296
Score: 296.00 Matches: 296
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.01% Indels: 0
Gaps: 15

US-09-719-272-1 (1-3467) x US-10-374-499-9 (1-296)

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QY 102 CCATCAGGAGTATGAGTCCGAGCAACATCGAGCGCTCAAGCCAAAGCCAAAGCCAAAGCCAA 161
Db 1 ProlethrAspLeuAlaAspAsnIleGluArgLeuLysAlaAsnAspGlyLeuLysPhe 20
QY 162 TCCAGGAGTATGAGTCCGAGCAACATCGAGCGCTCAAGCCAAAGCCAAAGCCAAAGCCAAAGCC 221
Db 21 SerGlnGluThrAspLeuAlaAspAsnIleGluArgLeuLysAlaAsnAspGlyLeuLysPhe 40
QY 222 GAGGTGAACAAAGCCAAAGCCAAAGCCAAAGCCAAAGCCAAAGCCAAAGCCAAAGCCAAAGCCAA 281
Db 41 GluValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHisSerArgVal 60
QY 282 ATCTTACCTCTATCGATGGCTCCCGGAGTGCATCATCGCTCAAGCCAAAGCCAAAGCCAAAGCCAA 341
Db 61 IleLeuThrSerIleAspGlyValProGlySerAspTyrIleAsnAlaAsnTyrIleAsp 80
QY 342 GGTACCGCAGCAAGATGCTACATCGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 401
Db 81 GlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGlyProLeuProGluThrMetGly 100
QY 402 GATTCTCGAGTATGAGTCCGAGCAACATCGAGCGCTCAAGCCAAAGCCAAAGCCAAAGCCAAAGCC 461
Db 101 AspPheTrpArgMetValTrpGluGlnArgThrAlaThrValValMetThrArgLeu 120
QY 462 GAGGAGAAAGTCCCGGGTAAATGTGATCAGTACGTGGCCAGCCCGTGGCCAGCCAGCCAGCCAGCC 521
Db 121 GluLysSerArgValLysCysAspGlnTyrTrpProAlaArgGlyThrGluThrCys 140
QY 522 GGCCTTATTCAGGTGACCTGTGTCGACGACGAGTGGAGTGGCCACATACATCTGTGCGCACC 581
```


Db 141 GlyLeuIleGlnValThrLeuLeuAspThrValGluLeuAlaThrThrValArgThr 160
2y 582 TTCGACTCCACAGAGTGGCTCAGTGAAGACCGTGGCTGCTCAGTTTCAGTTTCATG 541
Db 161 PheAlaLeuHisLysSerGlySerGluLeuArgGlnPheGlnPheMet 180
2y 642 GCTGGCCAGACCATGGAGTCTCAGTACCCCACTCCCATCTGCTGCTTCTTACGACGG 701
Db 181 AlaTrpProAspHisGlyValProGluThrProThrProIleLeuAlaPheLeuArgG 200
2y 702 GTCAGGCTTCGACCCCTAGACGCGAGGCCCATGGTGTGTGCTGACGAGCGGGCGTG 761
Db 201 ValLysAlaCysAsnProLeuAspAlaGlyProMetValHisCysSerAlaGlyVal 220
2y 762 GCGCGACCGCTGCTTCATCGTATTGATGCGCATGTTGGAGCGGATGAAGACACGAGAAG 821
Db 221 GlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluArgMetLysHISGLuLys 240
2y 822 ACGGTGACATCTATGCGCCACGTGACCTGATCGCATCACAGAGGAACATACATGTTGCGAG 881
Db 241 ThrValAspIleThrGlyHisValThrCysMetArgSerGlnArgAsnThrMetValGln 260
2y 882 ACGGAGACAGTACGTTTCATCCATGAGCGCTGCTGAGGCTGCCAGTCCGCGCCAC 941
Db 261 ThrGluAspGlnThrValPheIleHisGluAlaLeuLeuGluAlaAlaThrCysGlyHis 280
2y 942 ACAGAGTGGCTGCGCCGACCTGTATGTCACCATCCAGAGTGGCG 989
Db 281 ThrGluValProAlaArgAsnLeuThrAlaHisIleGlnLysLeuGly 296

RESULT 6

US-10-314-232-13
; Sequence 13, Application US/10314232
; Publication No. US20030138932A1
; GENERAL INFORMATION:
; APPLICANT: MOLLER, NIELS P.H.
; APPLICANT: MOLLER, KARIN B.
; APPLICANT: UELICH, AXEL
; TITLE OF INVENTION: PTP-531: A NOVEL PROTEIN TYROSINE PHOSPHATASE
; FILE REFERENCE: 038602/0886
; CURRENT APPLICATION NUMBER: US/10/314,232
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/361,096
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 08/449,609
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: 08/036,210
; PRIOR FILING DATE: 1995-03-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LAR
US-10-314-232-13

Alignment Scores:
Pred. No.: 1,23e-253 Length: 289
Score: 289.00 Matches: 289
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 25.40% Indels: 0
DB: 14 Gaps: 0

US-09-719-272-1 (1-3467) x US-10-314-232-13 (1-289)

Qy 81 ATGCGAGACCCACCCATCCCATCCGACCTGGCGGACACATCGAGCGCTCAA 140
Db 1 MetArgAspHisProPheIleProIleThrAspLeuAlaAspAsnIleGluArgLeuLys 20

Qy 141 GCCAACGATGGCTCAAGTTCTCCAGGAGTATGAGTCCATCCAGCCCTGGACAGCATTC 200
Db 21 AlaAsnAspGlyLeuLysPheSerGlnLysThrGluSerIleAspProGlyGlnPhe 40
Qy 201 ACGTGGAGATTCACAACTGGAGTGAAACAAGCCCAAGAACCGCTATGGAATGTCATC 260
Db 41 ThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArgTrpAlaAsnValle 60
Qy 261 CCCTACGACCACTCTCGAGTACCTTTACCTATCATCGATGGCTGCCGGGAGTACTAC 320
Db 61 AlaTrpAspHisSerArgValIleLeuThrSerIleAspGlyValProGlySerAspTr 80
Qy 321 ATCAATGCCAATCATCATCGTGTACCGCAACAGCAATACCTACATCCGACGAGGGC 380
Db 81 IleAsnAlaSerTrpIleAspGlyTrpArgLysGlnAsnAlaTrpIleAlaThrGlnGly 100
Qy 381 CCCGTGCCGACGACCATCGGCGATTTCTGGAGAATGTTGGGAACAGCGACGCGCACT 440
Db 101 ProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGluGlnArgThrAlaThr 120
Qy 441 GTGTCATGATGACACCGCTGGAGGAGAGTCCCGGGTAAATGTGATCAGTACTGTCACA 500
Db 121 ValValMetMetThrArgLeuGluGluLysSerArgValLysCysAspGlnTrpPro 140
Qy 501 GCCGTGGCACCCGAGACCTGTGGCTTTATTACAGGTGACCTGTTGGACACAGTGGAGCTG 560
Db 141 AlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrValGluLeu 160
Qy 561 GCCACATACATGTGGCGACCTTCGCACTCCACAGAGTGGCTCCAGTGAGAGCGTGAG 620
Db 161 AlaThrTrpValArgThrPheAlaLeuHisLysSerGlySerGluLysArgGlu 180
Qy 621 CTGCGTCAAGTTTCAGTTTCATGCGCTGCGCACCATGAGTTCCTGAGTACCCCACTCCC 680
Db 181 LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluThrPro 200
Qy 681 ATCTGGCTTCCTACGAGCGGTCAAGCGCTGCAACCCCTAGACGAGCGGCCCATGGTG 740
Db 201 IleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAspAlaGlyProMetVal 220
Qy 741 GTGCACTGACGCGGGCGTGGCGCGACCGCTGCTTCATCGTATGATGATGATGATG 800
Db 221 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeu 240
Qy 801 GAGCGGATGAAGACGAGAGAACGCGTGACATCATGCGCACGCTGACCTGCTGATCGATCA 860
Db 241 GluArgMetLysHisGluLysThrValAspIleThrValAspIleThrCysMetArgSer 260
Qy 861 CAGAGGAATCATGCTGTCAGACGAGGACGAGTACGTTGTTTCATCCATGAGCGCTGCTG 920
Db 261 GlnArgAsnThrMetValGlnThrGluAspGlnThrValPheIleHisGluAlaLeu 280
Qy 921 GAGGCTGCCACGTCGCGCCACACAGAG 947
Db 281 GluAlaAlaThrCysGlyHisThrGlu 289

RESULT 7

US-09-788-626-8
; Sequence 8, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 306
; TYPE: PRT

ORGANISM: Homo sapiens
US-09-788-626-8

Alignment Scores: 1.73e-174 Length: 306
Pred. No.: 202.00 Matches: 250
Percent Similarity: 97.66% Conservatives: 0
Best Local Similarity: 97.66% Mismatches: 0
Query Match: 17.75% Indels: 6
DB: 9 Gaps: 0

(S-09-719-272-1 (1-3467) x US-09-788-626-8 (1-306)

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195 CAGTTCAGTGGGAGGATTCACAACTGGAGGTCAACAGCCCAAGACCGCTATCGGAT 254
1 GlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArgTrpAlaAsn 20
255 GTCATGGCTTACACCACTCTCGAGTCATCTTACCTTATCGATGGCTCCCGGGAT 314
21 ValIleAlaTrpAspHisSerArgValIleLeuThrSerIleAspGlyValProGlySer 40
315 GACTACATCAATGCCAATCATCATGATGGCTACCGACGAGCAGATCCCTACATCGCCAG 374
41 AspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThr 60
375 CAGGGCCCTCGCCGAGACATGGCGATTCTCGAGATGGTGTGGAAACAGCGCAG 434
61 GlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGluGlnArgThr 80
435 GCCACTGTGTGATGATGAACAGCGGTGGAGGAGAGTCCCGGTAAATGTGATCATGATAC 494
81 AlaThrValValMetThrArgLeuGluGluLysSerArgValLysCysAspGlnTyr 100
495 TGCCAGCCCTGGCAGCAGATCGTGGCTTATTCAGGTGACCTGTGTGGACAGTG 554
101 TrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrVal 120
555 GAGCTGGCCACATACACTGTGGCAGCTTCGCACTCCACAGAGTGGCTCCAGTGAAG 614
121 GluLeuAlaThrTyrThrVal-----PheAlaLeuHisLysSerGlySerGluLys 138
615 CGTCAGTGGCTGATGTTTCAGTTCATGGCTGCCAGACCATGAGTTCCTGATGATCCCA 674
139 ArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrPro 158
675 ACTCCCATCTCTGGCTTCTTACAGCAGCGGTCAAGGCTTCAACCCCTAGACGAGGCCCC 734
159 ThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAspAlaGlyPro 178
735 ATGCTGGTGATCTCGAGGGGGGGCTGGCGCCAGCCGGCTCTCATCGTATGATGCC 794
179 MetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAla 198
795 ATGTTGGAGCGGATGAAGACGAGAAACGATGGACATCTATGGCCACGCTGATCGCATG 854
199 MetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisValThrCysMet 218
855 CGATCAGAGGAACTACATGGTGCAGAGGAGCAGACCATGATGTTTCATCCATGAGGGCG 914
219 ArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGluAla 238
915 CTGCTGGAGGCTGCCAGCTGGCGCCACACAGAGTG 950
239 LeuLeuGluAlaAlaThrCysGlyHisThrGluVal 250
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RESULT 8

US-09-788-626-27
Sequence 27, Application US/09788626
Patent No. US2002009762A1
GENERAL INFORMATION:
APPLICANT: Flint, Andrew J.
APPLICANT: Cool, Deborah G.
TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE

TITLE OF INVENTION: PHOSPHATES

FILE REFERENCE: 200125.401
CURRENT APPLICATION NUMBER: US/09/788,626
CURRENT FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 27

LENGTH: 294

TYPE: PRT

ORGANISM: Homo sapiens

US-09-788-626-27

Alignment Scores:

Pred. No.: 6.15e-170 Length: 294
Score: 197.00 Matches: 245
Percent Similarity: 97.61% Conservatives: 0
Best Local Similarity: 97.61% Mismatches: 0
Query Match: 17.31% Indels: 6
DB: 9 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-788-626-27 (1-294)

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1062 ACCTCCCGCTTCATCAGCGCCACCTGCAACAGTTCAAGAACCGCTGGTGAAC 1121
1 ThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsn 20
1122 ATCATGCCCTACGAATTGACCCCGTGTGTCTGCAGCCCCATCCGTGGTGTGGAGGGCTCT 1181
21 IleMetProTyrGluLeuThrArgValCysLeuGlnProIleArgGlyValGluGlySer 40
1182 GACTACATCATGCTCCAGCTTCCTGGATGTTATAGACAGAGGCGCTACATAGCTACA 1241
41 AspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnLysAlaTyrIleAlaThr 60
1242 CAGGGCCCTCGGCAGAGAGCAGCCAGAGACTTCTGGCGCATGTCTATGGAGCAATTC 1301
61 GlnGlyProLeuAlaGluSerThrGluAspPheTrpArgMetLeuTrpGluHisAsnSer 80
1302 ACCATATCTGTCATGTCACCAAGCTTCGGGAGATGGCAGGAGAAATGCCACCATAC 1361
81 ThrIleIleValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyr 100
1362 TGGCCAGCAGAGCGCTCTGCTCGCTACCAAGTACTTGTGTGTGACCCGATGGCTGAGTAC 1421
101 TrpProAlaGluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyr 120
1422 AACATGCCCGCAGTATATCTCGTGGTCAAGGTCAAGATGCCCGGATGGCAGTCA 1481
121 AsnMetProGlnTyrIleLeu-----PheLysValThrAspAlaArgAspGlyGlnSer 138
1482 AGGCAATCCGGCAGTTCACAGTTCACAGCTGGCCAGAGCGGCGTCCCAACACAGGC 1541
139 ArgThrIleArgGlnPheGlnPheThrAspTrpProGluGlnGlyValProLysThrGly 158
1542 GAGGGAATCATGCTTCATCGGCGAGTGCATAGACCAAGAGCGAGTTTGGACAGGAT 1601
159 GluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGluGlnPheGlyGlnAsp 178
1602 GGGCTATCATCGGTCCACTGTCAGTCTGGCTGGCGCGCCACCGGGTGTTCATCACTCTG 1661
179 GlyProIleThrValHisCysSerAlaGlyValGlyArgThrGlyValPheIleThrLeu 198
1662 AGCATCGCTCTGGAGCGCATGCGCTATGAGGGCGTGGTCGACATGTTTCAGACCGTGAAG 1721
199 SerIleValLeuGluArgMetArgTyrGluGlyValValAspMetPheGlnThrValLys 218
1722 ACCCTGGTACACAGCGTCTCCCATGCTGTCAGAGGAGCCAGATACAGCTGTGCTAC 1781
219 ThrLeuArgThrGlnArgProAlaMetValGlnThrGluAspGlnTyrGlnLeuCysTyr 238
1782 CGTGGCGGCTCGAGTACCTC 1802
239 ArgAlaAlaLeuGluTyrLeu 245
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RESULT 9

US-09-808-602-54

; Sequence 54, Application US/09808602

; Patent No. US20020155115A1

; GENERAL INFORMATION:

; APPLICANT: Vernet, Corine A

; APPLICANT: Fernandes, Elma

; APPLICANT: Shimkets, Richard A

; APPLICANT: Herrmann, John L

; APPLICANT: Majumder, Kumud

; APPLICANT: Mishra, Vishnu

; APPLICANT: Mezes, Peter S

; APPLICANT: MacDougall, John

; TITLE OF INVENTION: NO. US20020155115A1el Proteins and Nuclec Acids Encoding Same

; FILE REFERENCE: 15966-697 CIP

; CURRENT APPLICATION NUMBER: US/09/808,602

; CURRENT FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: 09/800,198

; PRIOR FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: 60/186,596

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 54

; LENGTH: 1502

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-808-602-54

Alignment Scores:

Pred. No.:	1.75e-44	Length:	1502
Score:	59.00	Matches:	59
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.18%	Indels:	0
DB:	9	Gaps:	0

US-09-719-272-1 (1-3467) x US-09-808-602-54 (1-1502)

QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGCGAGAGAAATGCCACCACTACTGCGCCAGCA 1370

Db 1331 ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyTrpProAla 1350

QY 1371 GAGCGCTCTGCTCGCTACAGTACTTTGTTGACCGATGGCTGAGTACAAATGCC 1430

Db 1351 GluArgSerAlaArgTyGlnTyPheValValAspProMetAlaGluTyAsnMetPro 1370

QY 1431 CAGTATATCTCGTGCAGTTCAGGTCAAGTCACGGATGCCGGGATGGCGCAGTCAAGGACA 1487

Db 1371 GlnTyIleLeuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArgThr 1389

RESULT 10

US-09-800-198-44

; Sequence 44, Application US/09800198

; Publication No. US20030087816A1

; GENERAL INFORMATION:

; APPLICANT: Vernet, Corine AM

; APPLICANT: Fernandes, Elma

; APPLICANT: Shimkets, Richard A

; APPLICANT: Herrmann, John L

; APPLICANT: Majumder, Kumud

; APPLICANT: Mishra, Vishna

; APPLICANT: Mezes, Peter S

; APPLICANT: Rastelli, Luca

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 15966-697

; CURRENT APPLICATION NUMBER: US/09/800,198

; CURRENT FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: 60/186,596

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 44

; LENGTH: 1502

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-800-198-44

Alignment Scores:

Pred. No.:	1.75e-44	Length:	1502
Score:	59.00	Matches:	59
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.18%	Indels:	0
DB:	10	Gaps:	0

US-09-719-272-1 (1-3467) x US-09-800-198-44 (1-1502)

QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGCGAGAGAAATGCCACCACTACTGCGCCAGCA 1370

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QY 1371 GAGCGCTCTGCTCGCTACAGTACTTTGTTGACCGATGGCTGAGTACAAATGCC 1430

Db 1351 GluArgSerAlaArgTyGlnTyPheValValAspProMetAlaGluTyAsnMetPro 1370

QY 1431 CAGTATATCTCGTGCAGTTCAGGTCAAGTCACGGATGCCGGGATGGCGCAGTCAAGGACA 1487

Db 1371 GlnTyIleLeuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArgThr 1389

RESULT 11

US-09-808-602-55

; Sequence 55, Application US/09808602

; Patent No. US20020155115A1

; GENERAL INFORMATION:

; APPLICANT: Vernet, Corine A

; APPLICANT: Fernandes, Elma

; APPLICANT: Shimkets, Richard A

; APPLICANT: Herrmann, John L

; APPLICANT: Majumder, Kumud

; APPLICANT: Mishra, Vishnu

; APPLICANT: Mezes, Peter S

; APPLICANT: MacDougall, John

; TITLE OF INVENTION: NO. US20020155115A1el Proteins and Nuclec Acids Encoding Same

; FILE REFERENCE: 15966-697 CIP

; CURRENT APPLICATION NUMBER: US/09/808,602

; CURRENT FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: 09/800,198

; PRIOR FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: 60/186,596

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 55

; LENGTH: 1948

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-808-602-55

Alignment Scores:

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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.18%	Indels:	0
DB:	9	Gaps:	0

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QY 1371 GAGCGCTCTGCTCGCTACAGTACTTTGTTGACCGATGGCTGAGTACAAATGCC 1430

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db 1797 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1816
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; 1431 CAGTATATCTCGTGGTCAAGTTCACAGTCCCGGATGGCGGATCAAGGACA 1487
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; 1817 GlnTyrIleLeuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArgThr 1835
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RESULT 12
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; JS-09-800-198-45
; Sequence 45, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Cornie AM
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrmann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishna
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15965-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 1948
; TYPE: PRT
; ORGANISM: Homo sapiens
; JS-09-800-198-45
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; Alignment Scores:
; Pred. No.: 1,69e-44 Length: 1948
; Score: 59.00 Matches: 59
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 5.18% Indels: 0
; Gaps: 0
; DB:
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; JS-09-719-272-1 (1-3467) x US-09-800-198-45 (1-1948)
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; 2y 1311 GTCATGCTGACCAAGCTTCGGAGATGGCAGGAGAAATGCCACAGTACTGGCCAGCA 1370
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; 1777 ValMetLeuThrLysLeuA-gGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1796
;
; 1371 GAGCGCTCTGCTCGCTACCAAGTACTTTGTTGACCCGATGCTGAGTACAAATGCC 1430
;
; 1797 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1816
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; 1431 CAGTATATCTCGTGGTCAAGTTCACAGTCCCGGATGGCGGATCAAGGACA 1487
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; 1817 GlnTyrIleLeuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArgThr 1835
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RESULT 13
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; JS-10-029-386-29636
; Sequence 29636, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AECOMICA-X-2 EXPRESSION ANALYSIS TWO
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 29636
; LENGTH: 57
; TYPE: PRT
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; JS-09-719-272-1 (1-3467) x US-10-029-386-29636 (1-57)
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; QY 476 CCGGACTTCTCCCTCCAGCCGTGTCTCATCATGACACACAGTGGCGCTGTTCACAC 417
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; Db 3 ProGlyLeuLeuLeuGlnProCysHisHisAspHisSerGlyArgAlaLeuPheProHis 22
;
; QY 416 CATTCCTCAGAAATCGCCCATGGTCTCGGAGAGGGCCCTCGTGGCGATGAGGCATT 357
;
; Db 23 HisSerProGluIleAlaHisGlyLeuGlyGlnGlyAlaLeuArgGlyAspValGlyIle 42
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; QY 356 CTGCTTGGGTAGCATCGATGTAGTTGGCATTGATGTAGTCACT 312
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; Db 43 LeuLeuAlaValAlaIleAspValValGlyIleAspValValThr 57
;
; RESULT 14
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; US-10-258-666-12
; Sequence 12, Application US/10258666
; Publication No. US20040005578A1
; GENERAL INFORMATION:
; APPLICANT: Yamada, Yoji
; APPLICANT: Sekine, Susumu
; APPLICANT: Kikuchi, Yasuhiro
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Kyowa Hakkō Kogyō Co., Ltd.
; TITLE OF INVENTION: Myocardial Cell Proliferation-Associated Genes
; FILE REFERENCE: 082382-000000US
; CURRENT APPLICATION NUMBER: US/10/258,666
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: JP 2000-126741
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: WO PCT/JP01/03700
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1495
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATRE:
; OTHER INFORMATION: RHDH-231, PTP-PI
; US-10-258-666-12
;
; Alignment Scores:
; Pred. No.: 3,39e-27 Length: 1495
; Score: 40.00 Matches: 40
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 3.51% Indels: 0
; Gaps: 0
; DB:
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; US-09-719-272-1 (1-3467) x US-10-258-666-12 (1-1495)
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; ORGANISM: Homo sapiens
; FEATRE:
; OTHER INFORMATION: MAP TO AC011772.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.95
; OTHER INFORMATION: SWISSPROT HIT: O00470, EVALUATE 1.20e+00
; US-10-029-386-29636
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; Alignment Scores:
; Pred. No.: 1,2e-40 Length: 57
; Score: 55.00 Matches: 55
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 4.86% Indels: 0
; Gaps: 14
; DB:
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; US-09-719-272-1 (1-3467) x US-10-029-386-29636 (1-57)
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; QY 476 CCGGACTTCTCCCTCCAGCCGTGTCTCATCATGACACACAGTGGCGCTGTTCACAC 417
;
; Db 3 ProGlyLeuLeuLeuGlnProCysHisHisAspHisSerGlyArgAlaLeuPheProHis 22
;
; QY 416 CATTCCTCAGAAATCGCCCATGGTCTCGGAGAGGGCCCTCGTGGCGATGAGGCATT 357
;
; Db 23 HisSerProGluIleAlaHisGlyLeuGlyGlnGlyAlaLeuArgGlyAspValGlyIle 42
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; QY 356 CTGCTTGGGTAGCATCGATGTAGTTGGCATTGATGTAGTCACT 312
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; Db 43 LeuLeuAlaValAlaIleAspValValGlyIleAspValValThr 57
;
; RESULT 14
;
; US-10-258-666-12
; Sequence 12, Application US/10258666
; Publication No. US20040005578A1
; GENERAL INFORMATION:
; APPLICANT: Yamada, Yoji
; APPLICANT: Sekine, Susumu
; APPLICANT: Kikuchi, Yasuhiro
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Kyowa Hakkō Kogyō Co., Ltd.
; TITLE OF INVENTION: Myocardial Cell Proliferation-Associated Genes
; FILE REFERENCE: 082382-000000US
; CURRENT APPLICATION NUMBER: US/10/258,666
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: JP 2000-126741
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: WO PCT/JP01/03700
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1495
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATRE:
; OTHER INFORMATION: RHDH-231, PTP-PI
; US-10-258-666-12
;
; Alignment Scores:
; Pred. No.: 3,39e-27 Length: 1495
; Score: 40.00 Matches: 40
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 3.51% Indels: 0
; Gaps: 15
; DB:
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; US-09-719-272-1 (1-3467) x US-10-258-666-12 (1-1495)
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Job time : 149 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

DN nucleic - protein search, using frame_plus_n2p model
Run on: March 9, 2004, 08:52:58 ; Search time 34.5 Seconds
(without alignments)
10465.347 Million cell updates/sec

Title: US-09-719-272-1
Perfect score: 1138
Sequence: 1 gatccgactgaaggactcc.....atttgataatcagattttc 3467

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Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 141681 seqs, 52070155 residues

Word size: 1

Total number of hits satisfying chosen parameters: 283186

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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-DB=SwissProt_42 -OPWT=fastan -SUFFIX=rsrp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
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-NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	607	53.3	1897	1 PTFP_HUMAN	P10586 homo sapien
2	59	5.2	1912	1 PTFD_HUMAN	P23468 homo sapien
3	59	5.2	1948	1 PTNS_HUMAN	Q13332 homo sapien
4	34	3.0	2029	1 LAR_DROME	P16621 drosophila
5	22	1.9	114	1 PT13_STYPL	P28205 styela plic
6	12	1.1	521	1 PT13_DICDI	P34137 dictyostell
7	12	1.1	699	1 PTFE_MOUSE	P49446 mus musculu
8	12	1.1	700	1 PTFE_HUMAN	Q03348 rattus norv
9	12	1.1	796	1 PTFR_RAT	P18433 homo sapien
10	12	1.1	802	1 PTFR_HUMAN	P18052 mus musculu
11	12	1.1	829	1 PTFR_MOUSE	P06800 mus musculu
12	12	1.1	1152	1 CD45_MOUSE	Q16825 homo sapien
13	12	1.1	1174	1 PTNL_HUMAN	Q62728 rattus norv
14	12	1.1	1175	1 PTNL_RAT	Q62136 mus musculu
15	12	1.1	1176	1 PTNL_MOUSE	Q62136 mus musculu
16	12	1.1	1187	1 PTNE_HUMAN	Q15678 homo sapien
17	12	1.1	1189	1 PTNE_MOUSE	Q62130 mus musculu
18	12	1.1	1255	1 CD45_RAT	P04157 rattus norv

19	12	1.1	1301	1 PTF9_DROME	P35832 drosophila
20	12	1.1	1304	1 CD45_HUMAN	P08575 homo sapien
21	12	1.1	1422	1 PTPG_CHICK	Q98936 gallus gall
22	12	1.1	1439	1 PTPG_HUMAN	Q15262 homo sapien
23	12	1.1	1454	1 PTPT_MOUSE	Q39m80 mus musculu
24	12	1.1	1463	1 PTFE_HUMAN	Q14522 homo sapien
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26	12	1.1	2314	1 PTFZ_HUMAN	Q62656 rattus norv
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29	11	1.0	550	1 PTP1_SCHPO	P27574 schizosacch
30	11	1.0	595	1 PTN6_HUMAN	P29350 homo sapien
31	11	1.0	711	1 PYP2_SCHPO	P2586 schizosacch
32	11	1.0	1216	1 PYP2_HUMAN	Q16827 homo sapien
33	11	1.0	1238	1 PTPJ_MOUSE	Q64455 mus musculu
34	11	1.0	1337	1 PTPJ_HUMAN	Q12913 homo sapien
35	11	1.0	1430	1 PTFU_HUMAN	Q92729 homo sapien
36	11	1.0	1442	1 PTPG_MOUSE	Q05909 mus musculu
37	11	1.0	1445	1 PTPG_HUMAN	P23470 homo sapien
38	11	1.0	1462	1 PTF6_DROME	P16620 drosophila
39	11	1.0	1705	1 PTFV_MOUSE	P70289 mus musculu
40	11	1.0	1711	1 PTFV_RAT	Q64612 rattus norv
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					P81718 rattus norv

ALIGNMENTS

RESULT 1
PTPF_HUMAN
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AC P10586;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48).
GN PTFPR OR LAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RX MEDLINE=89035978; PubMed=2972792;
RA Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.;
RT "A new member of the immunoglobulin superfamily that has a
cytoplasmic region homologous to the leukocyte common antigen.";
RL J. Exp. Med. 168:1523-1530(1988).
RN [2]
RP MUTAGENESIS.
RX MEDLINE=90046860; PubMed=2554325;
RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
RT "A family of receptor-linked protein tyrosine phosphatases in humans
and Drosophila.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
RN [3]
RP MUTAGENESIS.
RX MEDLINE=90316093; PubMed=1695146;
RA Streuli M., Krueger N.X., Tsai T., Tang M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like
domains of the receptor-linked protein tyrosine phosphatases LCA and
LAR.";
RL EMBO J. 9:2399-2407(1990).
CC -| FUNCTION: It is possible that DLAR is a cell adhesion receptor.
CC -| It possesses an intrinsic protein tyrosine phosphatase activity
(PTPase).
CC -| FUNCTION: The first PTPase domain has enzymatic activity, while
the second one seems to affect the substrate specificity of the
first one.

CC CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC CC tyrosine + phosphate.
CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC CC -!- SIMILARITY: Contains 8 fibronectin type III domains.
CC CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC CC
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CC CC or send an email to license@isb-sib.ch).
CC CC
CC CC -----
CC CC EMBL: Y00815; CAA68754.1; --
CC CC PIR: S03841; TDHULK
CC CC PDB: 1UAR; 25-APR-00.
CC CC Genes: HGNC:9670; PTPRF.
CC CC MIM: 179590; --
CC CC GO: GO:0005887; C: integral to plasma membrane; TAS.
CC CC GO: GO:0005001; P: transmembrane receptor protein tyrosine pho. .; TAS.
CC CC GO: GO:0007155; P: cell adhesion; TAS.
CC CC GO: GO:0007185; P: transmembrane receptor protein tyrosine pho. .; TAS.
CC CC InterPro: IPR008957; FN_III-like.
CC CC InterPro: IPR003961; FN_III.
CC CC InterPro: IPR003962; FNI subd.
CC CC InterPro: IPR007110; IG-like.
CC CC InterPro: IPR003598; IG C2.
CC CC InterPro: IPR003877; TYR phosphatase.
CC CC InterPro: IPR000242; Tyr_pp.
CC CC Pfam: PF00041; fa3; 7.
CC CC Pfam: PF00047; IG; 3.
CC CC Pfam: PF00102; Y phosphatase; 2.
CC CC PRINTS: PR00014; FNTYPEII.
CC CC PRINTS: PR00700; PTPPHPTASE.
CC CC SMART: SM00060; FN3; 4.
CC CC SMART: SM00408; IGc2; 3.
CC CC SMART: SM00194; PTPC; 2.
CC CC PROSITE: PS50835; IG-LIKE; 3.
CC CC PROSITE: PS00383; TYR PHOSPHATASE 1; 2.
CC CC PROSITE: PS50056; TYR PHOSPHATASE 2; 2.
CC CC PROSITE: PS50055; TYR PHOSPHATASE PTP; 2.
CC CC Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
CC CC Cell adhesion; Immunoglobulin domain; Repeat; 3D-structure.
CC CC SIGNAL 1 16
CC CC CHAIN 17 1897
CC CC LAR PROTEIN.
CC CC EXTRACELLULAR (POTENTIAL).
CC CC POTENTIAL.
CC CC CYTOPLASMIC (POTENTIAL).
CC CC IG-LIKE C2-TYPE 1.
CC CC IG-LIKE C2-TYPE 2.
CC CC IG-LIKE C2-TYPE 3.
CC CC PROTEIN-TYROSINE PHOSPHATASE 1.
CC CC PROTEIN-TYROSINE PHOSPHATASE 2.
CC CC PHOSPHOCYSTEINE INTERMEDIATE (BY
CC CC SIMILARITY).
CC CC PHOSPHOCYSTEINE INTERMEDIATE (BY
CC CC SIMILARITY).
CC CC ACT_SITE 1829 1829
CC CC CARBOHYD 107 107
CC CC CARBOHYD 240 240
CC CC CARBOHYD 285 285
CC CC CARBOHYD 711 711
CC CC CARBOHYD 956 956
CC CC CARBOHYD 1538 1538
CC CC MUTAGEN 1897 AA; 211844 MW; 439850FID5C031FF CRC64;
CC CC SEQUENCE 1897 AA; 211844 MW; 439850FID5C031FF CRC64;
CC CC

DB:	1	Gaps:	0
US-09-719-272-1 (1-3467) x PTPF_HUMAN (1-1897)			
QY	6	GAGCTGAGAGACTCTCTGCTGCGCCACTCTCTGAGCTCTGAGCTCTGAGAGTGGAGCTCAAC	65
Db	1291	GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgLeuAsn	1310
QY	66	TACACAGACCCAGGTATGCGAGACACCCACCCATCCCATCCAGCAGCTGGCGGACAAAC	125
Db	1311	TyrGlnThrProGlyMetArgAspHisProProIleThrAspLeuAlaAspAsn	1330
QY	126	ATCGAGCGCTCAAGCCAAAGATGGCTCAAGTCTCCAGAGGATGATGATCCATCGAC	185
Db	1331	IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleasp	1350
QY	186	CCTGGACAGCAGCTTCACTGGGAGAAATCAAACCTGGAGGTGAACAAGCCCAAGAACCGC	245
Db	1351	ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuValAsnLysProLysAsnArg	1370
QY	246	TATGGAGATGTCATCGCTAGACACACCTCTGAGTATCTCTTACCTCTATCGATGGCTC	305
Db	1371	TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal	1390
QY	306	CCCGGGAGTGACTACATCAATGCCAACTACATCGATGGCTACCGCAAGCAGAAATGCCTAC	365
Db	1391	ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr	1410
QY	366	ATCGCACAGCGGCCCCCTGCGGAGACCATGGCGATTTCTGGAGATGGTGTGGGAA	425
Db	1411	IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu	1430
QY	426	CAGCGCACGCGCCTGCTGATGATGACACGCGCTGGAGAGAGTCCCGGTAAAGT	485
Db	1431	GlnArgThrAlaThrValValMetMetThrArgLeuGluLysSerArgValLysCys	1450
QY	486	GATCAGTACTGCGCAGCGCGTGGCAGACCTGCGCTTATTCAGGTGACCCCTGTG	545
Db	1451	AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu	1470
QY	546	GACACAGTGGAGCTGCCACATACACTGTGCGACCTTCGCACTCCACAGAGTGGCTCC	605
Db	1471	AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer	1490
QY	606	AGTGAGAGCGTGAGCTGCGTGCAGTTTCAGTTTCATGGCTGCGCAGACCATGAGTTCT	665
Db	1491	SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro	1510
QY	666	GAGTACCCCACTCCATCTGCGCTTCTTACGAGCGGTCAAGGCTGCAACCCCTAGAC	725
Db	1511	GluTyrProThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAsp	1530
QY	726	GCAGGCGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	785
Db	1531	AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal	1550
QY	786	ATTGATGCCATGTTGAGCGGATGAAGACGAGAGAGCGGTGGACATCTATGCGCACGTG	845
Db	1551	IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal	1570
QY	846	ACCTGTCATGTCATCAGAGGAACATACATGTCGACAGCGAGGACCATGCTGTTTCATC	905
Db	1571	ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle	1590
QY	906	CATGAGCGCTGCTGAGCGTGCAGCTGCGGCGCACAGAGGTGCTGCGCGCACTG	965
Db	1591	HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu	1610
QY	966	TATGCCCATCCAGAGCTGGCGCAAGTCCCTCCAGGGGAGAGTGTGACCCCATGGAG	1025
Db	1611	TyrAlaHisIleGlnLysLeuGlnValProProGlyGluSerValThrAlaMetGlu	1630
QY	1026	CTCGAGTTCAAGTTGCTGGCGAGCTCAAGGCGCCACACGTCCTGCTTCATCGACGCCAAC	1085

Alignment Scores:
Pred. No.: 0
Score: 607.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 53.34%
Length: 1897
Matches: 607
Conservative: 0
Mismatches: 0
Indels: 0


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DR PRINTS: PRC0700; PRTPHPHTASE.
DR SMART; SM00194; PTP; 1.
DR PROSITE; PS00382; TYR PHOSPHATASE 1; 1.
DR PROSITE; PS00382; TYR PHOSPHATASE 2; 1.
DR PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
DR PROSITE; PS50055; TYR PHOSPHATASE_FTP; 1.
DR HYDROLASE.
FW FT DOMAIN 1 114 SER-RICH.
FW ACT_SITE 310 310 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT FT DOMAIN 327 425 PTPASE INSERT (ASN-RICH).
FT FT DOMAIN 382 400 POLY-ASN.
FT SEQUENCE 521 AA; 59427 MW; 0F516AEDD75EAB96 CRC64;
SQ

Alignment Scores:
Pred. No.: 0.00882 Length: 521
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: 1 Gaps: 0

US-09-719-272-1 (1-3467) x PTP1_DICDI (1-521)
QY 309 GGGAGTCACTACATCAATGCCAACTACATCGATGCG 344
DB 148 GlySerAspTyrIleAsnAlaAsnTyrIleAspGly 159

RESULT 7
PTPE_MOUSE STANDARD; PRT; 699 AA.
ID PTPE_MOUSE
DC P49446; Q62134; Q62444; Q64496;
AT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase epsilon precursor (EC 3.1.3.48) (R-PTP-
DE epsilon).
DN EPRE OR PTPE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RX MEDLINE=96064577; PubMed=7592814;
RA Elson A., Leder P.;
RT "Protein-tyrosine phosphatase epsilon. An isoform specifically
RT expressed in mouse mammary tumors initiated by v-Ha-ras OR neu."
RJ J. Biol. Chem. 270:26116-26122(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DEA/2;
RA Mukoyama Y.;
RT Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain, and Lung;
RA Hou E.W., Li S.L.;
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 224-332 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=93086603; PubMed=1454056;
RA Schepens J., Zeeuwen P., Wieringa B.;
RT "Identification and typing of members of the protein-tyrosine
RT phosphatase gene family expressed in mouse brain."
RL Mol. Biol. Rep. 15:241-248(1992).
RN [5]
RP SEQUENCE OF 224-332 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=95134232; PubMed=7832766;
RA Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
RT "A novel receptor-type protein tyrosine phosphatase with a single

```


RT catalytic domain is specifically expressed in mouse brain.";
RL Biochem. J. 305:499-504(1995).
CC -|- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC
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CC
CC EMBL; U33688; AAC52281.1; -;
DR EMBL; D83484; BAA11927.1; -;
DR EMBL; U62387; AAB04553.1; -;
DR EMBL; Z23052; CAA80587.1; -;
DR EMBL; Z23053; CAA80588.1; -;
DR PIR; B61180; B61180.
DR HSSP; P18052; 1YFO.
DR MGI; 97813; Ptpre.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr PP.
DR Pfam; PF00102; Y phosphatase; 2.
DR PRINTS; PR00700; RTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR PHOSPHATASE 1; 2.
DR PROSITE; PS00556; TYR PHOSPHATASE 2; 2.
DR PROSITE; PS00555; TYR PHOSPHATASE_FTP; 2.
KW Glycoprotein; Transmembrane; Hydroxylase; Phosphorylation; Repeat;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 699 PROTEIN-TYROSINE PHOSPHATASE EPSILON.
FT DOMAIN 20 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 68 POTENTIAL.
FT DOMAIN 69 699 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 153 392 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 393 699 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 334 334 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT ACT_SITE 629 629 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 500 500 G -> A (IN REF. 2).
FT CONFLICT 506 506 G -> V (IN REF. 2).
FT CONFLICT 521 522 IV -> ML (IN REF. 2).
FT CONFLICT 606 606 M -> I (IN REF. 1).
SQ SEQUENCE 699 AA; 80645 MW; 4D04467438017FEB CRC64;

Alignment Scores:
Pred. No.: 0.00839 Length: 699
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: 1 Gaps: 0

US-09-719-272-1 (1-3467) x PTPSE_MOUSE (1-699)
QY 738 GTGGTGACATGACGCGCGGCGTGGCGCCGACCGCG 773
|||
Db 331 ValValHisCysSerAlaGlyValGlyArgThrGly 342

RESULT 8
PTPE HUMAN
ID PTPE_HUMAN STANDARD; PRT; 700 AA.
AC P23469; Q96KQ6;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Protein-tyrosine phosphatase epsilon precursor (EC 3.1.3.48) (R-PTP-
DE epsilon).
GN PTPRE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=91006018; PubMed=2170109;
RA Krueger N.X., Streuli M., Saito H.;
RT "Structural diversity and evolution of human receptor-like protein
RT tyrosine phosphatases.";
RL EMBO J. 9:3241-3252(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC MEDLINE=22118122; PubMed=12121439;
RA Wabakken T.K., Hauge H., Finne E.F., Wiedlocha A., Aasheim H.C.;
RT "Expression of human protein tyrosine phosphatase epsilon in
RT leucocytes: a potential ERK pathway-regulating phosphatase.";
RL Scand. J. Immunol. 56:195-203(2002).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Sapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL -|- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
CC CYTOPLASMIC (isoform 2).
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P23469-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P23469-2; Sequence=VSP_007778;
CC -|- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X54134; CAA38069.1; -;
DR EMBL; AJ315969; CAC86583.1; -;
DR EMBL; BC050062; AAH50062.1; -;
DR PIR; S12053; S12053.
DR HSSP; P18052; 1YFO.
DR Genew; HGNC:9669; PTPRE.
DR MIM; 600926; -;

GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
 DR InterPro; IPR003595; PTPC motif.
 DR InterPro; IPR000387; Tyr_PTPase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00194; PTPC; 2.
 DR SMART; SM00404; PTPC motif; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE 2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;
 KW Signal; Alternative splicing.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 700 PROTEIN-TYROSINE PHOSPHATASE EPSILON.
 FT DOMAIN 20 46 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 47 69 POTENTIAL.
 FT DOMAIN 70 700 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 154 393 PROTEIN-TYROSINE PHOSPHATASE 1.
 FT DOMAIN 394 700 PROTEIN-TYROSINE PHOSPHATASE 2.
 FT ACT_SITE 335 335 PHOSPHOCYSTEINE INTERMEDIATE (BY
 FT ACT_SITE 630 630 SIMILARITY).
 FT ACT_SITE 630 630 PHOSPHOCYSTEINE INTERMEDIATE (BY
 FT SIMILARITY).
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 70 MEPCPLLVGVFSLFLARLGRNETTADSNETTTSPPDPF
 FT GASPLVLAALLPLLLVLLVLAAYFFR -> MSNRSSFS
 FT RLTV (in isoform 2).
 FT /FTid=VSP_007778.
 FT CONFLICT 516 516 E -> D (IN REF. 2).
 FT SEQUENCE 700 AA; 80641 MW; D096BCADCEA65708 CRC64;
 Alignment Scores:
 Pred. No.: 0.00839 Length: 700
 Score: 12.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: 1 Gaps: 0
 JS-09-719-272-1 (1-3467) x PTPC_HUMAN (1-700)
 ZY 738 GTGTGTCAGTCCAGCGGGCGTGGCGGCGACCGGC 773
 DB 332 ValValHisCysSerAlaGlyValGlyArgThrGly 343
 RESULT 9
 ID PTRA RAT STANDARD; PRT; 796 AA.
 AC Q03348;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-
 DE alpha).
 GN PTPRA OR LRP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OK NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93038682; PubMed=1417854;
 RA Moriwaya T., Fujiwara Y., Imai E., Takenaka M., Kawanishi S.,
 RA Inoue T., Noguchi T., Tanaka T., Kanada T., Ueda N.;
 RT "cDNA cloning of rat LRP, a receptor like protein tyrosine
 RT phosphatase, and evidence for its gene regulation in cultured rat
 RT mesangial cells."
 RL Biochem. Biophys. Res. Commun. 188:34-39(1992).
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein

tyrosine + phosphate.
 CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
 CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L01702; AAA1983.1; .
 DR HSP; F18052; IYFO.
 DR InterPro; IPR00387; Tyr_phosphatase.
 DR InterPro; IPR00242; Tyr_PP.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE 2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;
 KW Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 796 PROTEIN-TYROSINE PHOSPHATASE ALPHA.
 FT DOMAIN 20 145 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 146 169 POTENTIAL.
 FT DOMAIN 170 796 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 234 494 PROTEIN-TYROSINE PHOSPHATASE 1.
 FT DOMAIN 495 796 PROTEIN-TYROSINE PHOSPHATASE 2.
 FT ACT_SITE 436 436 PHOSPHOCYSTEINE INTERMEDIATE (BY
 FT SIMILARITY).
 FT ACT_SITE 726 726 PHOSPHOCYSTEINE INTERMEDIATE (BY
 FT SIMILARITY).
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 80 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 796 AA; 90260 MW; 4793796191056920 CRC64;
 Alignment Scores:
 Pred. No.: 0.00821 Length: 796
 Score: 12.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: 1 Gaps: 0
 US-09-719-272-1 (1-3467) x PTRA_RAT (1-796)
 QY 738 GTGTGTCAGTCCAGCGGGCGTGGCGGCGACCGGC 773
 DB 433 ValValHisCysSerAlaGlyValGlyArgThrGly 444
 RESULT 10
 ID PTRA_HUMAN STANDARD; PRT; 802 AA.
 AC P18433; Q14513; Q96TD9;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-
 DE alpha).
 GN PTPRA OR PTPA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CC NCBI_TaxID=9606;
 CC [1]
 CC SEQUENCE FROM N.A. (ISOFORM 3).
 CC MEDLINE=90349565; PubMed=2166945;
 CC RA Sap J., D'Eustachio P., Givol D., Schlessinger J.;
 CC "Cloning and expression of a widely expressed receptor tyrosine
 CC phosphatase.";
 CC Proc. Natl. Acad. Sci. U.S.A. 87:6112-6116(1990).
 CC [2]
 CC SEQUENCE FROM N.A. (ISOFORM 3).
 CC MEDLINE=90384936; PubMed=2169617;
 CC RA Kaplan R., Morse B., Huebner K., Croce C., Hawk R., Ravera M.,
 CC Ricca G., Jaye M., Schlessinger J.;
 CC "Cloning of three human tyrosine phosphatases reveals a multigene
 CC family of receptor-linked protein-tyrosine-phosphatases expressed in
 CC brain.";
 CC Proc. Natl. Acad. Sci. U.S.A. 87:7000-7004(1990).
 CC [3]
 CC SEQUENCE FROM N.A. (ISOFORM 4).
 CC MEDLINE=91006018; PubMed=2170109;
 CC RA Krueger N.X., Streuli M., Saito H.;
 CC "Structural diversity and evolution of human receptor-like protein
 CC tyrosine phosphatases.";
 CC EMBO J. 9:3241-3252(1990).
 CC [4]
 CC SEQUENCE FROM N.A. (ISOFORM 4).
 CC TISSUE=Kidney;
 CC MEDLINE=91088320; PubMed=2175890;
 CC RA Ohagi S., Nishi M., Steiner D.P.;
 CC "Sequence of a cDNA encoding human LRP (leukocyte common antigen-
 CC related peptide)."
 CC Nucleic Acids Res. 18:7159-7159(1990).
 CC [5]
 CC SEQUENCE FROM N.A. (ISOFORM 4).
 CC MEDLINE=91032191; PubMed=2172030;
 CC RA Jirik F.R., Janzen N.M., Melhado I.G., Harder K.W.;
 CC "Cloning and chromosomal assignment of a widely expressed human
 CC receptor-like protein-tyrosine phosphatase.";
 CC FEBS Lett. 273:239-242(1990).
 CC [6]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=91638749; PubMed=11780052;
 CC RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 CC Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
 CC Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 CC Beasley O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,
 CC Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,
 CC Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 CC Clegg S., Cobley V.E., Collier R.E., Connor R.E., Dunn M.,
 CC Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 CC Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 CC Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 CC Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 CC Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 CC Kay M.P., Kimberley A.M., King A.E., Jekosch K., Johnson C.M., Johnson D.,
 CC Leleasaliho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 CC Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,
 CC Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 CC Oliver K., Parker A., Patel R., Pearce T.V., Peck A.I.,
 CC Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 CC Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
 CC Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 CC Swann R.M., Sycamore A.C., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 CC Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
 CC Whitehead S.I., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 CC Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 CC Rogers J.;
 CC "The DNA sequence and comparative analysis of human chromosome 20.";
 CC Nature 414:865-871(2001).
 CC RA Nature 414:865-871(2001).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=4;
 Name=1; Synonyms=Long;
 IsoId=PI8433-1; Sequence=Displayed;
 Name=2; Synonyms=Short;
 IsoId=PI8433-2; Sequence=VSP_005145;
 Name=3;
 IsoId=PI8433-3; Sequence=VSP_007776; VSP_007777;
 Name=4;
 IsoId=PI8433-4; Sequence=VSP_007777;
 -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
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 or send an email to license@isb-sib.ch).
 EMBL; M34668; AAA36528.1; -
 EMBL; X54130; CAA38065.1; -
 EMBL; X54890; CAA38682.1; -
 EMBL; X53364; CAA37447.1; -
 EMBL; AL121905; CAC10336.1; -
 EMBL; AL121905; CAC10337.1; -
 PIR; A36065; A36065.
 HSP; P18052; 1YFO.
 Genew; HGNC:9664; PTPRA.
 MIM; 176884; -
 GO; GO:0005887; C:integral to plasma membrane; TAS.
 GO; GO:0005000; P:transmembrane receptor protein tyrosine pho. . . ; TAS.
 InterPro; IPR003595; PTPC motif.
 InterPro; IPR003987; TYR_PhoPhatase.
 InterPro; IPR00242; Tyr PP.
 Pfam; PF00102; Y_PhoPhatase; 2.
 PRINTS; PR00700; PRTYPHPHTASE.
 SMART; SM00194; PTPC; 2.
 SMART; SM00404; PTPC_motif; 2.
 PROSITE; PS00393; TYR_PHOSPHATASE_1; 2.
 PROSITE; PS00556; TYR_PHOSPHATASE_2; 2.
 PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 2.
 GlycoProtein; Transmembrane; Hydrolase; Phosphorylation; Signal;
 Repeat; Alternative splicing.
 SIGNAL 1 19
 CHAIN 20 802
 DOMAIN 20 142
 TRANSMEM 143 185
 DOMAIN 166 802
 DOMAIN 241 500
 DOMAIN 501 802
 ACT_SITE 442 442
 FT ACT_SITE 732 732
 FT CARBOHYD 21 21
 FT CARBOHYD 36 36
 FT CARBOHYD 68 68
 FT CARBOHYD 80 80
 FT CARBOHYD 86 86
 FT CARBOHYD 104 104
 FT CARBOHYD 124 124
 FT VARSPIC 139 147
 FT VARSPIC 138 138
 FT VARSPIC 179 187
 FT CONFLICT 114 114
 FT CONFLICT 122 122
 FT CONFLICT 289 289
 FT CONFLICT 367 367
 FT CONFLICT 493 493
 FT CONFLICT 786 786

SQ SEQUENCE 802 AA; 90599 MW; 8E964C3B5B5B32 CRC64;

Alignment Scores: 0.0082 Length: 802
Pred. No.: 12.00 Matches: 12
Score: 100.00% Conservatives: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 1.05% Gaps: 0
DB:

US-09-719-272-1 (1-3467) x PTR_A_HUMAN (1-802)

Qy 738 GTGTCGACTGACGGCGGCGTGGCGGCGACCGGC 773

Db 439 ValValHisCysSerAlaGlyValGlyArgThrGly 450

RESULT 11

PTR_A_MOUSE

ID PTR_A_MOUSE STANDARD; PRT; 829 AA.

AC P18052; Q61808;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-PEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-
alpha) (LCA-related phosphatase).
GN PTR_A OR LRP OR PTR_A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6 X DBA/2;
RX MEDLINE=90280391; PubMed=2162042;
RA Matthews R.J., Cahir E.D., Thomas M.L.;
RT "Identification of an additional member of the protein-tyrosine-
phosphatase family: evidence for alternative splicing in the tyrosine
phosphatase domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:4444-4448(1990).
RN [2]
RP SEQUENCE OF 358-467 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=95134232; PubMed=7832766;
RA Hendriks W., Schepens J., Bruygan C., Zeeuwen P., Wieringa B.;
RT "A novel receptor-type protein tyrosine phosphatase with a single
catalytic domain is specifically expressed in mouse brain.";
RL Biochem. J. 305:499-504(1995).
RN [3]
RP SEQUENCE OF 651-756 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=93086603; PubMed=1454056;
RA Schepens J., Zeeuwen P., Wieringa B., Hendriks W.;
RT "Identification and typing of members of the protein-tyrosine
phosphatase gene family expressed in mouse brain.";
RL Mol. Biol. Rep. 16:241-248(1992).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 202-503.
RX MEDLINE=96320562; PubMed=8700232;
RA Bilwes A.M., den Hertog J., Hunter T., Noel J.P.;
RT "Structural basis for inhibition of receptor protein-tyrosine
phosphatase-alpha by dimerization.";
RL Nature 382:555-559(1996).

CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P18052-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P18052-2; Sequence=VSP 005146;
CC -1- TISSUE SPECIFICITY: Widely expressed.
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

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CC

DR EMBL; M36033; AAA39448.1; -
DR EMBL; M36034; AAA39449.2; -
DR EMBL; Z23054; CAA80589.1; -
DR EMBL; Z23055; CAA80590.1; -
DR PIR; A47373; A47373.
DR PDB; 1YFO; 01-APR-97.
DR MGD; MGI:97808; Btpra.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000442; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Signal;
KW Repeat; Alternative splicing; 3D-structure.
FT SIGNAL 1 19 PROBABLE.
FT CHAIN 20 829 PROTEIN-TYROSINE PHOSPHATASE ALPHA.
FT DOMAIN 20 142 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 143 166 POTENTIAL.
FT DOMAIN 167 829 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 232 527 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 528 829 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 469 469 PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
FT ACT_SITE 759 759 PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 47 47 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 80 80 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 124 124 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 268 303 Missing (in isoform Short).
FT FTIG=VSP 005146.
SQ SEQUENCE 829 AA; 93697 MW; 7B1E335D4CC8B09B CRC64;

Alignment Scores:

Pred. No.: 0.00816 Length: 829
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: 1 Gaps: 0

US-09-719-272-1 (1-3467) x PTR_A_MOUSE (1-829)

Qy 738 GTGTCGACTGACGGCGGCGTGGCGGCGACCGGC 773

Db 466 ValValHisCysSerAlaGlyValGlyArgThrGly 477

RESULT 12

CD45_MOUSE

ID_CD45_MOUSE STANDARD; PRT; 1152 AA.

AC P06800;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (lymphocyte

DE common antigen Ly-5) (CD45) (T200).

GN PTPRC OR LY-5.

CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X79510; CA56042.1; -
 CC PIR: I38140; I38140.
 CC DR HSSP; Q06124; 2SHP.
 CC DR Genew; HGNC:9651; PTPN21.
 CC DR MIM; 603271; -
 CC DR GO; GO:0005856; C:cytoskeleton; TAS.
 CC DR GO; GO:0004725; F:protein tyrosine phosphatase activity; TAS.
 CC DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
 CC DR InterPro; IPR000299; Band 4.1
 CC DR InterPro; IPR000387; TYR_P. Phosphatase.
 CC DR InterPro; IPR000242; TYR_PP.
 CC DR Pfam; PF00373; Band_41; 1.
 CC DR Pfam; PF00102; Y_phosphatase; 1.
 CC DR PRINTS; PR00335; BAND41.
 CC DR PRINTS; PR00700; PRTYPHPTASE.
 CC DR SMART; SM00295; B41; 1.
 CC DR SMART; SM00184; PTPC; 1.
 CC DR PROSITE; PS00660; FERM_1; 1.
 CC DR PROSITE; PS00661; FERM_2; 1.
 CC DR PROSITE; PS00577; FERM_3; 1.
 CC DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 CC DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
 CC DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
 CC DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
 CC DR Structural protein; Cytoskeleton; Hydroxylase.
 CC FM DOMAIN 23 308 FERM.
 CC FT DOMAIN 921 1174 PROTEIN-TYROSINE PHOSPHATASE.
 CC FT ACT_SITE 1108 1108 PHOSPHOCYSTEINE INTERMEDIATE
 CC (BY SIMILARITY).
 CC FT DOMAIN 340 343 POLY-PRO.
 CC FT DOMAIN 565 574 POLY-PRO.
 CC FT DOMAIN 712 717 POLY-GLU.
 CC SO SEQUENCE 1174 AA; 133287 MW; 5772D9B1A9B3FDA CRC64;
 Alignment Scores:
 Pred. No.: 0.0077 Length: 1174
 Score: 12.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 Gaps: 0
 DB: 1
 US-09-719-272-1 (1-3467) x PTNL_HUMAN (1-1174)
 QY 1614 GTGCACTGAGTGTGGCGTGGCGGACCGGGG 1649
 Db 1106 VALHSCYSEERALAGLYVALGTYRGTHRGIV 1117
 RESULT 14
 PTNL_RAT
 ID PTNL_RAT STANDARD; PRT; 1175 AA.
 AC Q62728; Q62728; (Rel. 35. Created)
 DT 01-NOV-1997 (Rel. 35. Last sequence update)
 DT 10-OCT-2003 (Rel. 42. Last annotation update)
 DE Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase 2E).
 GN PTPN21 OR PTP2E.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxId=10116;
 RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2E).
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=9510449; PubMed=7805871;
 RA L'Abbe D., Banville D., Tong Y., Stocco R., Masson S., Ma S.,
 RA Fanus G., Shen S.H.;
 RT Identification of a novel protein tyrosine phosphatase with sequence
 RT homology to the cytoskeletal proteins of the band 4.1 family.";
 RL FEBS Lett. 356:351-356(1994).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q62728-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q62728-2; Sequence=VSP 000498;
 CC -1- TISSUE SPECIFICITY: Particularly abundantly in adrenal glands.
 CC -1- SIMILARITY: Contains 1 FERM domain.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U17971; AA62153.1; -
 CC EMBL: U18293; AA62154.1; -
 CC DR PIR; S51005; S51005.
 CC DR HSSP; Q06124; 2SHP.
 CC DR InterPro; IPR000299; Band 4.1.
 CC DR InterPro; IPR000387; TYR_P. Phosphatase.
 CC DR InterPro; IPR000242; TYR_PP.
 CC DR Pfam; PF00373; Band_41; 1.
 CC DR Pfam; PF00102; Y_phosphatase; 1.
 CC DR PRINTS; PR00335; BAND41.
 CC DR PRINTS; PR00700; PRTYPHPTASE.
 CC DR SMART; SM00295; B41; 1.
 CC DR SMART; SM00194; PTPC; 1.
 CC DR PROSITE; PS00660; FERM_1; 1.
 CC DR PROSITE; PS00661; FERM_2; 1.
 CC DR PROSITE; PS00577; FERM_3; 1.
 CC DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 CC DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
 CC DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
 CC DR Structural protein; Cytoskeleton; Hydroxylase; Alternative splicing.
 CC FM DOMAIN 23 308 FERM.
 CC FT DOMAIN 922 1175 PROTEIN-TYROSINE PHOSPHATASE.
 CC FT ACT_SITE 1109 1109 PHOSPHOCYSTEINE INTERMEDIATE
 CC (BY SIMILARITY).
 CC FT VARSPLIC 1 839 Missing (in isoform 2E).
 CC FT FTID=VSP 000498.
 CC SO SEQUENCE 1175 AA; 133411 MW; 82A684FC0F5EECF7 CRC64;
 Alignment Scores:
 Pred. No.: 0.00769 Length: 1175
 Score: 12.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 Gaps: 0
 DB: 1
 US-09-719-272-1 (1-3467) x PTNL_RAT (1-1175)
 QY 1614 GTGCACTGAGTGTGGCGTGGCGGACCGGGG 1649
 Db 1107 VALHSCYSEERALAGLYVALGTYRGTHRGIV 1118
 RESULT 15
 PTNL_MOUSE

ID PTNL_MOUSE STANDARD; PRT; 1176 AA.
AC Q62136;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase PTP-RL10).
GN PTPN21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=95140431; PubMed=783837;
RA Higashitsuji H., Arai S., Furutani M., Imamura M., Kaneko Y.,
RA Takenawa T., Nakayama H., Fujita T.,
RT "Enhanced expression of multiple protein tyrosine phosphatases in the
RT regenerating mouse liver: isolation of PTP-RL10, a novel cytoplasmic-
RT type phosphatase with sequence homology to cytoskeletal protein
RT 4.1.";
RL Oncogene 10:407-414(1995).
CC -1- FUNCTION: May be involved in the regulation of growth and
CC differentiation of liver cells.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- TISSUE SPECIFICITY: Liver.
CC -1- SIMILARITY: Contains 1 FERM domain.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.

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DR EMBL; D37801; BAA07053.1; -
DR PIR; I58345; I58345.
DR HSSP; P29350; IGWZ.
DR MGD; MG1:1344406; Ptpn21.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyx_PP.
DR Pfam; PF00373; Band 41; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM_1; 1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS50057; FERM_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00385; TYR_PHOSPHATASE_FTP; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR structural protein; Cytoskeleton; Hydrolyase.
KW structural protein; Cytoskeleton; Hydrolyase.
FT DOMAIN 23 308 FERM.
FT DOMAIN 923 1176 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1110 1110 PHOSPHOCYSTEINE INTERMEDIATE
FT FT 343 POLY-PRO.
FT DOMAIN 340 343 POLY-PRO.
FT DOMAIN 365 372 POLY-PRO.
SQ SEQUENCE 1176 AA; 133490 MW; 529FBE22F1335B75 CRC64;

Alignment Scores:

Pred. No.: 0.00769 Length: 1176
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.05% Indels: 0
DB: 1 Gaps: 0
US-09-719-272-1 (1-3467) x PTNL_MOUSE (1-1176)
QY 1614 GTGCACTGCGAGTGTGCGCGGCGCGCACCGGAGTG 1649
DB 1108 ValHecysSerAlaGlyValGlyArgGlnGlyVal 1119

Search completed: March 9, 2004, 09:04:25
Job time : 72.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 9, 2004, 08:56:18 ; Search time 168 Seconds

(without alignments)
13022.638 Million cell updates/sec

Title: US-09-719-272-1

Perfect score: 1138
Sequence: 1 gattccgactgaagactcc.....atttgataatcagatttct 3467

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2033934

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEBL-frame+ n2p-model -DEV=x1p
-Q=/cgr2_1/USPRO.spool_P/US09719272/runat_09032004_085230_7450/app_query.fasta_1.3655
-DB=SPREMBL_25 -QPMT=fastan -SUFFIX=spc -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=psco
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US09719272 @CGN 1.1 188 @runat_09032004_085230_7450 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEIOENTRY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

1: SPREMBL_25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirts:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	580	51.0	1191	4	Q723X4 homo sapien

2	506	44.5	1898	4	Q86WS0	Q86WS0 homo sapien
3	259	22.8	460	11	Q62917	Q62917 rattus norv
4	259	22.8	1887	11	Q9QW67	Q9QW67 rattus sp.
5	254	22.3	1898	11	Q64604	Q64604 r protein-t
6	250	22.0	582	11	Q64696	Q64696 mus musculu
7	172	15.1	1788	13	Q91AJ0	Q91AJ0 xenopus lae
8	160	14.1	1898	13	Q9E017	Q9E017 mus musculu
9	135	11.9	508	13	Q90X25	Q90X25 brachydanio
10	106	9.3	468	13	Q91B55	Q91B55 potamorygo
11	59	5.2	140	11	Q62590	Q62590 rattus norv
12	59	5.2	192	11	Q8C922	Q8C922 mus musculu
13	59	5.2	398	11	Q62604	Q62604 rattus norv
14	59	5.2	468	13	Q91BA2	Q91BA2 potamorygo
15	59	5.2	468	13	Q91BA0	Q91BA0 potamorygo
16	59	5.2	615	13	Q91A18	Q91A18 xenopus lae
17	59	5.2	749	11	Q8R169	Q8R169 mus musculu
18	59	5.2	857	13	Q90Y74	Q90Y74 brachydanio
19	59	5.2	1254	11	Q8VBV0	Q8VBV0 mus musculu
20	59	5.2	1399	4	Q75870	Q75870 homo sapien
21	59	5.2	1499	13	Q9C015	Q9C015 gallus gall
22	59	5.2	1501	11	Q9QW00	Q9QW00 rattus sp.
23	59	5.2	1501	11	Q7T117	Q7T117 mus musculu
24	59	5.2	1502	4	Q9UM61	Q9UM61 homo sapien
25	59	5.2	1863	11	Q64605	Q64605 rattus norv
26	59	5.2	1896	13	Q91AJ1	Q91AJ1 xenopus lae
27	59	5.2	1904	11	Q64699	Q64699 mus musculu
28	55	4.8	469	5	Q9NL11	Q9NL11 branchiost
29	46	4.0	1231	5	Q17024	Q17024 anopheles g
30	45	4.0	1894	11	Q64487	Q64487 mus musculu
31	44	3.9	89	4	Q16343	Q16343 homo sapien
32	44	3.9	154	11	Q63847	Q63847 mus musculu
33	40	3.5	1437	5	Q44329	Q44329 hirudo medi
34	38	3.3	469	13	Q9NL08	Q9NL08 epitalretus
35	34	3.0	383	5	Q8MTNO	Q8MTNO culicoides
36	34	3.0	1597	5	Q96OM3	Q96OM3 dirosophila
37	34	3.0	2029	5	Q9V188	Q9V188 dirosophila
38	30	2.6	79	11	Q8CC23	Q8CC23 mus musculu
39	30	2.6	93	11	Q8CC54	Q8CC54 mus musculu
40	25	2.2	468	13	Q9NL06	Q9NL06 epitalretus
41	25	2.2	472	13	Q9NL02	Q9NL02 epitalretus
42	25	2.2	2051	5	Q44328	Q44328 hirudo medi
43	18	1.6	63	13	Q9Q949	Q9Q949 gallus gall
44	15	1.3	471	5	Q9Y1X6	Q9Y1X6 ephydaria f
45	15	1.3	488	5	Q9NL12	Q9NL12 branchiost

ALIGNMENTS

RESULT 1
ID Q723X4 PRELIMINARY; PRT; 1191 AA.
AC Q723X4;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686B1310 (Fragment).
GN DKFZP686B1310.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Human cervix;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Podo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX537361; CAD97607.1; -
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 1191 AA; 134914 MW; 8320FEEDDADAC278 CRC64;

Alignment Scores:

Pred. No.: 0 Length: 1191
 Score: 580.00 Matches: 580
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.97% Indels: 0
 Gaps: 0

US-09-719-272-1 (1-3467) x Q723X4 (1-1191)

QY 6 GGAAGTGAAGAGTCTGCTGGCCCACTCTGACCCCTGAGAGTGGAGGCTCAAC 65
 Db 585 Gtyleuylaspserrleuualahlserrserasprovalglimechrglrleuasm 604
 QY 66 TACCAAGACCCAGATATGCGAGCAACCCCATCCCATCAGCACTGGCGGCAAC 125
 Db 605 Tylglnthrprogllymetaragaspheisprocollethrapsleuualaspsn 624
 QY 126 ATCGAGGCGCTCAAGCAAGATGGCCCTCAAGTTCTCCAGAGATATGAGTCAATGAC 185
 Db 625 llegluargleuylasasaspsgllyleuylspseserglnlglutylserlleasp 644
 QY 186 CCTGACAGACAGTTCACGTGGAGAAATTCAACTGAGAGTGAACAGCCCAAGACCGC 245
 Db 645 Progllylnlphethrtrpdlunseraserleuualasnllyprolyasasng 664
 QY 246 TATGCAATGTCAATGCTTACGACCACTCTGAGATCACTTACTTATGATGGCGTC 305
 Db 665 Tylalaaasvalillealatrapsheiserasvalilleethrserilleaspllyal 684
 QY 306 CCCGAGAGTACTATCAATGCAATGCCAATCATGATGAGTACCGCAAGCAAGATGCCAC 365
 Db 685 Progllyseraspllyrilleasnlasentylilleaspllyltyarlgylglasnlalatr 704
 QY 366 ATGCGCAAGCAGGCGCCCTGCGCCCAAGACCAATGGCGGATTTTGGAGAAATGGTGGAA 425
 Db 705 lilealathrlngllyproleuproglnthmetgllyaspphetrparmetvalitrlpdlu 724
 QY 426 CAGCGCAGGCACTGTGTGATGATGACACGGCTGGAGAGAAATCCCGGGTAAAGT 485
 Db 725 Glnargrthralthrvalalmetethrargleuulglulysethrlyalyscys 744
 QY 486 GATCAGTACTGGCCAGCCCGTGGACCCAGACCTTGGCTTATTCAGGTGACCTGTGTG 545
 Db 745 Aspglnltyrtrpcolalargllythrgrluthrlysgllyleuulglilvalthrleuenu 764
 QY 546 GACACAGTGGAGTGGCCATATCACTGAGGCACTTGGACCTGCAAGAGAGGCTCC 605
 Db 765 Asprthrvalgluleuualthrlythrvalargthrphalaleuualyserserlyser 784
 QY 606 ACTGAGAGCGTGAAGCTGGTCAATTCATGATTCAGTGGCCAGACCATGAGTTCT 665
 Db 785 SerglulysarlglnleuualarglnpneginpneumetalatrpProaspheisgllyalPro 804
 QY 666 GAGTACCCCACTCCCTGCTGCTTCTTCAAGAGCGGGTCAAGGCTTGAACCCCTTAC 725
 Db 805 GlulyrzprothrprolleuualapneueuargvalylvalaspsnProleuasp 824
 QY 726 GAGAGGCCCATGATGCTGACATGACAGCGGCGTGGCGGCAAGCGGTGCTTCACTG 785
 Db 825 AlaglylPrometValalHlscyserrlagllyalgllyargthrngllycyspherlleval 844
 QY 786 ATTGATGCCATGTTGGAGGAGTGAAGCAAGCAAGAGCGGTGGAATCTATAGGCCACTG 845
 Db 845 lileasplalmetleuualargmetcllyshlsiglulysrthrvalasplllyrcllyal 864
 QY 846 ACTGCATGCAATCAAGAGAACTACATGCTGACAGACGAGCAAGCAAGTCACTGTTCA 905
 Db 865 ThrlyserMetArgserlnlrgasentylmetvalglntnrglulaspglntlyrValphelle 884
 QY 906 CATGAGCGCTGTGAGGCTGCGACAGTGGCGGCAACAGAGAGTCTCGCCGCAACTG 965
 Db 885 HlsglualaleuulglualalathrlysgllylstrnglulvalProalargasnlenu 904

QY 966 TATGCCACATCCAGAGAGTGGGCCAAGTGCCTCCAGGGAGAGTGAACCCCATGAG 1025
 Db 905 TylalahlsllelglulysleuulglulvalProprogllyglulserValthrleuueglu 924
 QY 1026 CTGAGATTCAGTGTGCGCCAGCTCCAGGCCCAACAGTCCCGCTTCAATCAGCGCAAC 1085
 Db 925 Leuulphelyleuulaleuualaserlysalahstrserargphelleaserlisaen 944
 QY 1086 CTGCGCTGCAAGATTCAGAAACCGGCGTGTGAACATGATGCGCTTCAAGTCAACCGCT 1145
 Db 945 LeuproclyasnllyshelysasnlargleuualasnllemeProtyrcluleuthrarg 964
 QY 1146 GTGTGTGACCCCATCCGTGTGAGAGGCTGTGACTTCAATCAATGCCAGTTCTGTG 1205
 Db 965 ValCysleuulnleprolleargllyalglulysersaspllyrilleasnlaserPheleu 984
 QY 1206 GATGTTATGACAGAGAGAGGCTTCAATGATGACACAGGGCGCTTGGACAGAGCAC 1265
 Db 985 Aspllyltyrarglulnlysalatylrillealathngllyproleuualglulserthr 1004
 QY 1266 GAGACCTTCTGGGCAATGCTATGGAGCAATTCACCATCATGCTCATGCTGACCAAG 1325
 Db 1005 GluaspphetrpargmethleutrpdluHlsasenserrthllelvalMetleuthrlyls 1024
 QY 1326 CTTCGGGAGATGGCGAGGAGAAATGCCACAGTCTGGCCGACAGAGCGCTGTGCTGC 1385
 Db 1025 LeuarglulmetllyarglulyscyslsglntlyrtrpProalglulargserlialag 1044
 QY 1386 TACAGACTTGTGTTGATACCGGATGAGTGTGATACMAATGCCAGATATTCCTGCT 1445
 Db 1045 TylglnltyrthelvalalaspProemeralaglulryasmeProglntlyrilleuualg 1064
 QY 1446 GAGTTCAGAGTCAAGATGCCAGATCCGGGATGGCGAGTCAAGCAATCCGAGATTCAGATTC 1505
 Db 1065 Gluphelyvalthrapsalargaspsgllylnserasglthrillearglulnleuulnpe 1084
 QY 1506 ACAGACTGGCCAGAGAGAGGCGGTGCCAAGAGAGGAGGATTCATGACTTCAATCCGG 1565
 Db 1085 ThrasprtrprodlulnlyalProlysthrngllyglulylPheilleaspherlleglly 1104
 QY 1566 CAGGTGATTAAGCAAGAGAGATTTGAGACAGATGGCGCTTATCAGGTGACCTGCACT 1625
 Db 1105 GlnvalahlsythrlysglulnleuualargllylnaspsgllyProillethrvalahlsyser 1124
 QY 1626 GCTGCGTGGCGGCGGACCGGGGTTCATCACTGAGAGATGCTTGGAGGCAATGGCGC 1685
 Db 1125 AlaglylvalcllyargthrngllyalPheillethrleuualserllevalleuulargmetarg 1144
 QY 1686 TATGAGGCGGTGTGACATGTTTCAGACCGTGAAGACCTTCGTCACAGGCTCTGCTGCC 1745
 Db 1145 TylglnllyalvalalaspmetpneginthrlysthrleuualargthrGlnarproala 1164

RESULT 2

ID Q86WS0 PRELIMINARY, PRT, 1898 AA.

AC Q86WS0;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)
 DE Protein tyrosine phosphatase, receptor type, F
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo
 CN NCBI TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bye;
 RA Stranberg R;
 RT Submitted (MAR-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC048768; AAH48768.1;
 DR GO; GO:0005634; C:cytosol; IEA;
 DR GO; GO:0003677; F:DNA binding; IEA;
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR GO: 00004872; F:receptor activity; IEA.
DR GO: 0006470; P:protein amino acid dephosphorylation;
DR InterPro: IPR003962; FNIII_subd.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003598; IG_c2.
DR InterPro: IPR001005; MY5_DNA_binding.
DR InterPro: IPR003595; PTPc_mec1l.
DR InterPro: IPR000387; Tyr_phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PFO0041; fn3_7.
DR Pfam: PFO0047; IG_3.
DR Pfam: PFO0102; Y_phosphatase; 2.
DR PRINTS: PR00014; ENTYPHEP11.
DR PRINTS: PR00700; ENTYPHEP1ASE.
DR SMART: SM00060; FN3; 8.
DR SMART: SM00409; IG; 3.
DR SMART: SM00408; IGc2; 3.
DR SMART: SM00194; PTPc; 2.
DR SMART: SM00404; PTPc_mec1f; 2.
DR PROSITE: PSS50835; MYB_1; 1.
DR PROSITE: PSS00037; MYB_1; 1.
DR PROSITE: PSS00383; Tyr_PHOSPHATASE_1; 2.
DR PROSITE: PSS50056; Tyr_PHOSPHATASE_2; 2.
DR PROSITE: PSS50055; Tyr_PHOSPHATASE_PTP; 2.
DR Receptor.
SQ SEQUENCE 1898 AA; 211673 MW; 03AE355624C2FFA7 CRC64

DB 1812 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1831

QY 1626 GCTGGCGTGGCGCCGACCGGGGTGTTCATCACTTGAGCATGCTCTGGAGCGCATGGC 1685

DB 1832 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1851

QY 1686 TATAGAGGCGGTGGTGGCATGTTTCAGACCGTGAAGACCTGGCGTACACAGCGTCTGGCC 1745

DB 1852 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnAlaGlyProAla 1871

QY 1746 ATGGTGCAGACAGACGACCACTATCACTGTGTACCGTGGCGGCTTGAGTACTTGGC 1805

DB 1872 MetValGlnThrGluAspGlnTyrGlnLeuGlyTyrArgAlaAlaLeuGlnTyrLeuGly 1891

QY 1806 AGCTTTGACCACTATGCAACG 1826

DB 1892 SerPheAspHisTyrAlaThr 1898

RESULT 3

062917 PRELIMINARY; PRT; 460 AA.

AC Q62917. PRELIMINARY; PRT; 460 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE IAR receptor-linked tyrosine phosphatase.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxId=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague Dawley; TISSUE=Brain;

RX MEDLINE=94075340; PubMed=8253779;

RA Longo P.M., Martignetti J.A., Le Beau J.M., Zhang J.S., Barnes J.P., Brosius J.

RT "Leukocyte common antigen-related receptor-linked tyrosine phosphatase. Regulation of mRNA expression."

RL J. Biol. Chem. 268:26503-26511(1993).

DR EMBL: U00477; AAC04306.1; -.

DR PIR: A56493; A56493.

DR HSSP: P18052; 1YFO.

DR GO: GO:0016787; F:hydrolase activity; IEA.

DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR GO: GO:0004872; F:receptor activity; IEA.

DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.

DR InterPro: IPR000387; Tyr_P.

DR InterPro: IPR000242; Tyr_PP.

DR Pfam: PF00102; Y_phosphatase; 2.

DR PRINTS: PR00700; ERYPHPTASE.

DR SMART: SM00194; PTPC; 2.

DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.

DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 2.

DR PROSITE: PS00055; TYR_PHOSPHATASE_FTP; 2.

KW Hydrolase; Receptor.

SQ SEQUENCE 460 AA; 52989 MW; B78C8E504F1260FA CRC64;

Alignment Scores:

Pred. No: 1,13e-256 Length: 460

Score: 259.00 Matches: 259

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 22.76% Indels: 0

DB: 11 Gaps: 0

US-09-719-272-1 (1-3467) x Q62917 (1-460)

QY 1050 TCAGAGCCCAACAGTCCGCTTCATGAGCCCAAGTCCCTGCAAGAGTTCAGAGAC 1109

DB 202 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAlaHisPheLysAsn 221

QY 1110 CGGCTGTGAACATCATGCCCTAGATGACCGGTGTGTGTGAGGCCATCCGTGCT 1169

DB 222 ArgLeuValAsnIleMetProTyrGluLeuThrArgValLysLeuGlnProIleArgGly 241

QY 1170 GTGAGGGCTCTGACTCATCAATGACGAGCTTCCTGATGGTTATAGACAGAGAGGCC 1229

DB 242 ValGluGlySerAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnLysAla 261

QY 1230 TACATAGCTACAGAGGGCTCTGGCAGAGAGACCCAGAGACTTCTGGCGCATGCTATG 1289

DB 262 TyrIleAlaThrGlnGlyProLeuAlaGluSerThrGluAspPheTrpArgMetLeuTrp 281

QY 1290 GAGCACTTCACCATCATGATGTCATGTCGCAAGCTCGGGAGATGGCAGAGAGAAA 1349

DB 282 GluHisAsnSerThrIleIleValMetLeuThrLysLeuArgGluMetGlyArgGluLys 301

QY 1350 TGCCACAGTACTGGCCGACAGAGCGCTCTGCTGCTACCACTTCTTTGTTGACCCG 1409

DB 302 CysHisGlnTyrTrpProAlaGluArgSerAlaArgTyrGlnTyrPheValAlaAspPro 321

QY 1410 ATGGCTGAGTCAACATGCGCCAGATATCTGCGTGGAGTCAAGTCAAGTCAAGTCCCG 1469

DB 322 MetAlaGluTyrAsnMetProGlnTyrIleLeuArgGluPheLysValThrAspAlaArg 341

QY 1470 GATGGCACTCAAGAGACATCGGAGCTTCACAGTTCACAGACTGGCCAGAGAGCGCTG 1529

DB 342 AspGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGluGlnGlyVal 361

QY 1530 CCCAGACAGGAGGAGTTTCACTTCACTTCAGGAGGAGTAAAGCAAGAGAGAG 1589

DB 362 ProLysThrGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThrLysGluGln 381

QY 1590 TTGGACAGAGATGGGCTTATCAAGTGCATGACATGCTGCGGCGGCGGCGAGCGGCTG 1649

DB 382 PheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArgThrGlyVal 401

QY 1650 TTCATCACTTGAACATGCTCTGAGAGGAGCATGCGCTTGAAGGCGGTGGAGCATGTT 1709

DB 402 PheIleThrLeuSerIleValLeuGlnArgMetArgTyrGlnGlyValValAspMetPhe 421

QY 1710 CAGACCGTGAAGACCTGGCTACACAGGCTCTGTCATGTTGACAGACAGAGACGAT 1769

DB 422 GlnThrValLysThrLeuArgThrGlnArgProAlaMetValGlnThrGluAspGlnTyr 441

QY 1770 CAGCTGTGCTACCGTGGCGGCTTGAGTACTTGGCAGCTTGAACCATGATGCAAG 1826

DB 442 GlnLeuGlyTyrArgAlaAlaLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr 460

RESULT 4

090W67 PRELIMINARY; PRT; 1887 AA.

AC 090W67. PRELIMINARY; PRT; 1887 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE IAR, leukocyte common antigen-related PROTEIN=TRANSMEMBRANE receptor phosphotyrosine phosphatase.

OS Rattus sp. Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxId=10118;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=92278755; PubMed=1317540;

RX Yu Q., Lenardo T., Weinberg R.A.;

RT "The N-terminal and C-terminal domains of a receptor tyrosine phosphatase are associated by non-covalent linkage."

RL Oncogene 7:1051-1057(1992).

DR HSSP: P18052; 1YFO.

DR GO: GO:0005634; C:nucleus; IEA.

DR GO: GO:0003677; F:DNA binding; IEA.

DR GO: GO:0016787; F:hydrolase activity; IEA.

DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR GO: GO:0006470; F:protein amino acid dephosphorylation; IEA.

DR InterPro: IPR003962; Pnlti_subd.

DR InterPro: IPR003961; FN III.
 DR InterPro: IPR008957; FN III-like.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003968; IG_c2.
 DR InterPro: IPR001005; MYB_DNA_binding.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; TYR_PP.
 DR Pfam: PF00041; fn3; 7.
 DR Pfam: PF00047; Ig; 3.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00014; FNTYPE1IT.
 DR PRINTS: PR00700; FRTYPEPHATSE.
 DR SMART: SM00060; FN3; 6.
 DR SMART: SM00408; IGc2; 2.
 DR SMART: SM00194; PTPc; 2.
 DR PROSITE: PS50835; IG_LIKE; 3.
 DR PROSITE: PS00037; MYE_1; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTF; 2.
 DR HydroLase: Immunoglobulin domain; Repeat.
 KW SEQUENCE 1887 AA; 210453 MW; B84B33E7E4E70281 CRC64;

Alignment Scores:
 Pred. No.: 9 36e-257 Length: 1887
 Score: 259.00 Matches: 259
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 22.76% Indels: 0
 DB: 11 Gaps: 0

US-09-719-272-1 (1-3467) x Q9QW67 (1-1887)

QY 1050 TCAGAGGCCACACAGTCCCGCTTCATGACGCCACCTGCTGCAACAGTTCAAGAAC 1109
 DB 1629 SerlysalahisthrSerArgpheiLeSerAlahamLeuProCySaenlySpheLySaen 1648
 QY 1110 CGGCTGTGAACATCATCATGCTCCCTAGCAATGACCCGCTGTGTCTGACGCCACCTGCTG 1169
 DB 1649 ArgLeuValaenilleMeMetProtyrGluLeuThrArgValaCySaenGlnProIleArgGly 1668
 QY 1170 GTGAGGGGCTCTGACTCATCATCATGCTCCCTGATGATGATTATAGACAGAAAGCC 1229
 DB 1669 ValGluGlySerAspYrTyrLeaenAlaSerPheLeuaspGlyTyrArgGlnGlnlySa 1688
 QY 1230 TACATAGCTACACAGGGGCTCTGCGACAGACGCCAGACTTTCGGCCATGCTATGG 1289
 DB 1689 TyrLeaIatHrGlnGlyProLeuAlaGluSerThrGluaspPheTTPArgMetLeuTyr 1708
 QY 1290 GAGCACAATTCACCATCATCATGCTGCTGACCAAGCTTCGGAGATGGGACGAGAA 1349
 DB 1709 GluHisasnSerThrIleIleValaMetLeuThrIysLeuArgGluMetGlyArgGly 1728
 QY 1350 TGCCACCACTACCTGCGACGAGAGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1409
 DB 1729 CysHisGlnTyrTyrProAlaGluArgSerAlaArgTyrGlnTyrPheValValaAspPro 1748
 QY 1410 ATGCTGAGTACCAATGAGCCAGTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1469
 DB 1749 MetIaGluTyrAsnMetProGlnTyrIleLeuArgGluPheValIleHisValIleHisVal 1768
 QY 1470 GATGGGAGTCAAGACCAATCCGAGCTTCAGTTCAACAAGCTTCGCGACAGAGAGCGGTG 1529
 DB 1769 AspGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTyrProGluGlnGlyVal 1788
 QY 1530 CCCAAGACAGGAGGAGGATTCATGACTTCATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1589
 DB 1789 ProlystHrGlyGluGlyPheIleAspPheIleGlyIleValIleHisValIleHisVal 1808
 QY 1590 TTGAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1649
 DB 1809 PheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArgThrGlyVal 1828

QY 1650 TTCATCACTCTGAGCATGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1709
 DB 1829 PheIleThrLeuSerIleValaLeuGluArgMetArgTyrGluGlyValaValaAspMetPhe 1848
 QY 1710 CAGACCTGAGAACCTCTGCTGACACAGGCTTCGATGCTGACACAGACAGACAGACAGTAT 1769
 DB 1849 GlnThrValIleThrLeuArgThrGlnArgProAlaMetValGlnThrGluAspGlnTyr 1868
 QY 1770 CAGCTGTGCTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1826
 DB 1869 GlnLeuCytyrArgAlaAlaLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr 1887

RESULT 5
 Q64604 PRELIMINARY; PRT; 1898 AA.
 AC Q64604; Q63294; Q63295; Q63296; Q63297; Q63298; Q63299; Q63300; Q63301; Q63302; Q63303; Q63304; Q63305; Q63306; Q63307; Q63308; Q63309; Q63310; Q63311; Q63312; Q63313; Q63314; Q63315; Q63316; Q63317; Q63318; Q63319; Q63320; Q63321; Q63322; Q63323; Q63324; Q63325; Q63326; Q63327; Q63328; Q63329; Q63330; Q63331; Q63332; Q63333; Q63334; Q63335; Q63336; Q63337; Q63338; Q63339; Q63340; Q63341; Q63342; Q63343; Q63344; Q63345; Q63346; Q63347; Q63348; Q63349; Q63350; Q63351; Q63352; Q63353; Q63354; Q63355; Q63356; Q63357; Q63358; Q63359; Q63360; Q63361; Q63362; Q63363; Q63364; Q63365; Q63366; Q63367; Q63368; Q63369; Q63370; Q63371; Q63372; Q63373; Q63374; Q63375; Q63376; Q63377; Q63378; Q63379; Q63380; Q63381; Q63382; Q63383; Q63384; Q63385; Q63386; Q63387; Q63388; Q63389; Q63390; Q63391; Q63392; Q63393; Q63394; Q63395; Q63396; Q63397; Q63398; Q63399; Q63400; Q63401; Q63402; Q63403; Q63404; Q63405; Q63406; Q63407; Q63408; Q63409; Q63410; Q63411; Q63412; Q63413; Q63414; Q63415; Q63416; Q63417; 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CC	ISolid=Q64604-2; Sequence=VSP_050409, VSP_050410, VSP_050413,
CC	Name=PRLAR4.0;
CC	ISolid=Q64604-3; Sequence=VSP_050415;
CC	Name=PRLAR18.1;
CC	ISolid=Q64604-4; Sequence=VSP_050414, VSP_050415;
CC	Name=PRLARCB9;
CC	ISolid=Q64604-5; Sequence=VSP_050411, VSP_050412;
CC	-1- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL OR
CC	NERVOUSCULAR TISSUE
CC	-1- DEVELOPMENTAL STAGE: THE ALTERNATIVELY SPLICED ISOFORMS ARE
CC	DEVELOPMENTALLY REGulated.
CC	-1- SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-LIKE
CC	DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS), AND A
CC	CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS (BY SIMILARITY).
DR	EMBL; L11586; AAC37655.1; -
DR	EMBL; M60103; AAA41510.1; -
DR	EMBL; X83505; CA58495.1; -
DR	EMBL; X83546; CA58537.1; -
DR	PIR; S46216; S46216.
DR	HSSP; P18052; 1YFO.
DR	GO; GO:0016021; C: integral to membrane; IEA.
DR	GO; GO:0005194; F: cell adhesion molecule activity; IEA.
DR	GO; GO:0016787; F: hydrolase activity; IEA.
DR	GO; GO:0004727; F: prenylated protein tyrosine phosphatase act. ; IEA
DR	GO; GO:0004873; F: receptor activity; IEA.
DR	GO; GO:0007155; P: cell adhesion; IEA.
DR	GO; GO:0006470; P: protein amino acid dephosphorylation; IEA.
DR	InterPro; IPR003962; FNIII_stud.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR008957; FN_III-like.
DR	InterPro; IPR007110; I9-1-like.
DR	InterPro; IPR003598; I9_c2.
DR	InterPro; IPR000387; TYR_phosphatase.
DR	InterPro; IPR000242; TYR_pp.
DR	Pfam; PF00041; fn3; 7.
DR	Pfam; PF00047; I9; 3.
DR	Pfam; PF00102; Y_phosphatase; 2.
DR	PRINTS; PR00014; FNTYPEIII.
DR	PRINTS; PR00700; PRTPHPPTASE.
DR	SMART; SM00060; FN3; 6.
DR	SMART; SM00408; IGC2; 2.
DR	SMART; SM00194; PTPC; 2.
DR	PROSITE; PS50835; IG_LIKE; 3.
DR	PROSITE; PS00583; TYR_PHOSPHATASE_1; FALSE_NEG.
DR	PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR	PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW	Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
KW	Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.
FT	SIGNAL
FT	CHAIN
FT	28 1898
FT	27
FT	POTENTIAL.
FT	PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-
FT	TYPE. P POLYPEPTIDE.
FT	EXTRACELLULAR (POTENTIAL).
FT	POLY-ARG.
FT	POTENTIAL.
FT	CYTOPLASMIC (POTENTIAL).
FT	IG-LIKE C2-TYPE DOMAIN.
FT	IG-LIKE C2-TYPE DOMAIN.
FT	IG-LIKE C2-TYPE DOMAIN.
FT	FIBRONECTIN TYPE-III.
FT	FIBRONECTIN TYPE-III.
FT	PROTEIN-TYROSINE PHOSPHATASE.
FT	PROTEIN-TYROSINE PHOSPHATASE.
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	POTENTIAL.
FT	POTENTIAL.
FT	POTENTIAL.
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD
FT	941 941

FT	CARBOHYD	957	957	N-LINKED (GLCNAC,) (POTENTIAL).
FT	VARSPLIC	600	707	CTKQSPAPSPQVCTVSGSTVTSVTSVTPSPADSPNGLIT
FT				QYSVALEAVDGBGRKRVVDGSTRHSVSDVLDEKTEYR
FT				VWVRHATIDVGPGESSPVVTRDEDV -> RTAQSM (in
FT				isoform PRLAR631).
FT	VARSPLIC	771	771	/Frid=VSP 050409.
FT				Q -> QMRPESSEDY (in isoform PRLAR631).
FT				/Frid=VSP 050410.
FT	VARSPLIC	810	810	A -> AGE (in isoform PRLARCB9).
FT				/Frid=VSP 050411.
FT	VARSPLIC	811	1898	Missing (in isoform PRLARCB9).
FT				/Frid=VSP 050412.
FT	VARSPLIC	812	1004	Missing (in isoform PRLAR631).
FT				/Frid=VSP 050413.
FT	VARSPLIC	1276	1276	K -> KSKOE (in isoform PRLAR18.1).
FT				/Frid=VSP 050414.
FT	VARSPLIC	1316	1316	G -> GSNASNCNBS (in isoform PRLAR4.0).
FT				isoform PRLAR631 and isoform PRLAR18.1).
FT				/Frid=VSP 050415.
FT	MUTAGEN	1539	1539	C -> S (IN REF. 2).
FT	CONFLICT	777	777	T -> S (IN REF. 2 AND 3).
FT	CONFLICT	1073	1073	I -> T (IN REF. 2 AND 3).
FT	CONFLICT	1434	1434	G -> N (IN REF. 2 AND 3).
FT	CONFLICT	1639	1639	RA -> HT (IN REF. 2 AND 3).
FT	CONFLICT	1643	1644	
FT	SEQUENCE	1898 AA;	211492 NM;	DPADT46F5896F4B CAC64;

Alignment Scores:			
Pred. No.:	1,33e-251	Length:	1898
Score:	254.00	Matches:	254
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	22.32%	Indels:	0
DB:	11	Gaps:	0

US-09-719-272-1 (1-3467) x Q64604 (1-1898)			
QY	1065	TCCGCTTCATGACGCGCAACCTGCGGAGCAAGTTCAAGAACTGGCTGTGAACATC	1124
DB	1645	SETRPHEIIESSRLAENUEPCYASMLYSHEYSARMLAGLUEVALASMLE	1664
QY	1125	ATGCCCTTGCAGATTGACCCGCTGTGTGTGTCAGCCCATCGTGTGTGAGAGGCTCTGCAC	1184
DB	1665	MECPROYRIULNEUTNRARGVALCYLLENGINPROLEIARGLYVALIGLUGLYSERASP	1684
QY	1185	TACATGCATGCGACCTTCGGAGGTATATGACAGAGAGAGGCTCATAGTACACAG	1244
DB	1665	TYRIIEANALASEPHELEUASPGLYTYRARGINGINLSALATYRIIEALETHGLN	1704
QY	1245	GAGCCTTGCAGAGAGAGACCGAGACATCTTGCGCATGCTATGGAGACCAATTCCAC	1304
DB	1705	GLYPROLEUALAGLUSERTHGLIASPHERETPRGMETLEUTRPGIUNHASMSERTHR	1724
QY	1305	ATCATGCGCATGCGACCAACCTTCGGAGATGAGGAGAGAGATGCGACCACTACTCG	1364
DB	1725	ILEIIEVALMETLEUINMLYSEUARGIUNETGLYARGIULSYCYSHISGLINTYTRP	1744
QY	1365	CCAGCAGAGCGCTGTCTGCTGCTACCAAGTACTTGTGTGAACCCGATGCTGAAGTACAAC	1424
DB	1745	PROIAGIUAARGSERIALARGTYGLINTYRHEVALVALASPROMETALAGIULTRYASN	1764
QY	1425	ATGCCCGCATATACCTGCGTGAAGTTCAAGGTACCGATGCGCGGAGATGGGACGTCAAG	1484
DB	1765	MECPROGINTRYRIIELEUARGIUNPHEYSVALTHIRASPLAARGASPGLYGINSETRARG	1784
QY	1485	ACAAATCGGCACTTCAGTTCAAGACTGGCCCAAGCAGGCGGTGCCCAAGCAGCGCAG	1544
DB	1785	THIRIEARGINPHEGLINPHETHRASPTRPROGINDINGLYVALPROLYETHRGLYGLN	1804
QY	1545	GAATTCATTGATTCATCGGGAGAGGTGACATAGACAGAGAGAGATTGGACAGAGATGGG	1604
DB	1805	GLYPHEIIEASPHIEIIEGLYVALHISLYSTHRYLSGLINGINPHEGLYGLINASPOLY	1824

QY 1617 CACTGAGTGTGCTGCGCCGACCGGGGTTCATCACTGTGAGCATGCTGTGAG 1676
 Db 513 Hicyserraliaglyalglargthrglyvalpheliehrleuserilvalleuglu 532
 QY 1677 CGATGCGCTATGAGGCGCGTGTGCACTGTTCACACCGTGAAACCTGCTGACAG 1736
 Db 533 ArgMeaArgTyrGluglyalValAspMetPheGlnThrValThreLeuArgThrGln 552
 QY 1737 CGTCTGCGCATGGTGACAGACAGACCAAGTATCACTGTGTCACTGCGCGCTGAG 1796
 Db 553 ArgProAlaMetValGlnThrGlnAspGlnThrLeuGlyCysTyrArgAlaAlaLeuGlu 572
 QY 1797 TACCTGCGACGCTTTGACCACTATGCAACG 1826
 Db 573 TyrLeuGlySerPheAspHisTyrAlaThr 582

RESULT 7

Q91AJ0 PRELIMINARY; PRT; 1788 AA.

AC Q91AJ0; 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Receptor protein tyrosine phosphatase IAR.
 GN XPRP-IAR.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20193505; PubMed=10727868;
 RA Johnson K.G., Holt C.E.;
 RT "Expression of CRP-alpha, IAR, PTP-delta, and PTP-rho in the
 RT developing xenopus visual system."
 RL Mech. Dev. 92:291-294(2000).
 DR HSSP; AF:97945; AAF43606.1; -
 DR HSSP; P18052; 1YFO.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR007110; IG c2.
 DR InterPro; IPR003598; IG c2.
 DR InterPro; IPR000387; Tyr_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; Fn3; 7.
 DR Pfam; PF00047; Ig; 3.
 DR Pfam; PF0102; Y_phosphatase; 2.
 DR SMART; SMO0060; FN3; 7.
 DR SMART; SMO0408; IGC2; 3.
 DR SMART; SMO0194; PTPC; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 KM Hydrolyase; Immunoglobulin domain; Repeat.
 SQ SEQUENCE 1788 AA; 200271 MW; AB19254986D9067 CRC64;

Alignment Scores:

Pred. No.: 3,34e-167 Length: 1788
 Score: 172.00 Matches: 172
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 15, 11% Indels: 0
 DB: 13 Gaps: 0

US-09-719-272-1 (1-3467) X Q91AJ0 (1-1788)

QY 1311 GTGATGCTGACCAAGCTTCGGAGATGGGAGAGAGAAATGCCACCAAGTACTGGCAGCA 1370

Db 1617 ValMetLeuThrTyrLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1636
 QY 1371 GAGGCTCTGCTGCTACCAAGTACTTTGTTGACCCGACGTGAGTACCAAGTACGCC 1430
 Db 1637 GlnArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGlnTyrAsnMetPro 1656
 QY 1431 CAGTATATCTGCGTGAAGTTCAAGTCAAGATGCCGAGATGGGAGTCAAGACATC 1490
 Db 1657 GlnTyrLeuArgGluPheLysValThrAspAlaArgAspGlyLysSerArgThrIle 1676
 QY 1491 CGGAGTTTCCAGTTTCAAGACTGCCAGACAGGCGGTGCCCAAGACAGGATTC 1550
 Db 1677 ArgGlnPheGlnPheThrAspTyrProGlnGlnGlyValProLysThrGlnGlnGlyPhe 1696
 QY 1551 ATTGACTTCATCGGCGAGGTGATTAAGACCAAGACAGAGATTGAGACAGATGCCCTATC 1610
 Db 1697 IleAspHeiLeuGlnValHisLysThrLysGlnGlnPheGlnLysAspGlyProIle 1716
 QY 1611 ACGGTGACATGTCATGCTGTGCGCGCGGACCGGAGGTGTTCATCACTGTGACATCCTC 1670
 Db 1717 ThrValHisCysSerAlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleVal 1736
 QY 1671 CTGAGAGCGCATGCGCTATGAGCGGTGTGCAATGTTTCAACCGTGAACCTGTGCGCT 1730
 Db 1737 LeuGlnArgMetArgTyrGlnGlyValValAspMetPheGlnThrValLysThrLeuArg 1756
 QY 1731 ACACAGGCTTCCTGCGCATGTGTGACAGACAGACCAAGTATCACTGTGCTACCTGTGCGCC 1790
 Db 1757 ThrGlnArgProAlaMetValGlnThrGlnAspGlnTyrGlnLeuGlyCysTyrArgAlaAla 1776
 QY 1791 CTGAGTACCTCGGACGCTTTGACCACTATGCAACG 1826
 Db 1777 LeuGlnTyrLeuGlySerPheAspHisTyrAlaThr 1788

RESULT 8

Q9EQ17 PRELIMINARY; PRT; 1898 AA.

AC Q9EQ17; 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Tyrosine phosphatase IAR.
 GN XPRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=21135493; PubMed=11241288;
 RA Terzowski G., Jankowski A., Hendriks W.J.A.J., Rolink A.G.,
 RA Kistelow P.;
 RT "Within the hemopoietic system, IAR phosphatase is a T cell lineage-
 RT specific adhesion receptor-like protein whose phosphatase activity and
 RT function."
 RL Eur. J. Immunol. 31:832-840(2001).
 DR EMBL; AF300943; AAC40194.1; -
 DR HSSP; P18052; 1YFO.
 DR MGD; MGI:102695; PPRF.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003962; FNIII subd.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR007110; IG c2.
 DR InterPro; IPR003598; IG c2.
 DR InterPro; IPR000387; Tyr_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; Fn3; 7.
 DR Pfam; PF00047; Ig; 3.

DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00014; FNTYPEPHTI.
DR PRINTS: PR00700; FRTYPEPHTASE.
DR SMART: SM00060; FN3; 6.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS50835; IG LIKE; 3.
DR PROSITE: PS50833; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Hydrolyase; Immunoglobulin domain; Repeat.
KW SEQUENCE 1898 AA; 211504 MW; EFD48DD1B352A4A CRC64;

Alignment Scores:

Pred. No.:	7,456-155	Length:	1898
Score:	160.00	Matches:	160.
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	14.06%	Indels:	0
DB:	11	Gaps:	0

US-09-719-272-1 (1-3467) x Q90YJ5 (1-1898)

QY	1077	AGCGGCAACCTGCTGCAACAGTTCAAGAACCGGCTGTGGAACATCATGCGCTAGGA	1136
DB	1649	SerialaenLeupProCyAsnlysephelysasnlygLeuValaenlleMeleProlyGlu	1668
QY	1137	TTGACCCGTGTGTCTGACAGCCCATCCGCTGTGTGAGGGCTCTGACTCATCATGACC	1196
DB	1669	LeuthrargValCysleuglnProlearglValgluglySseraerpyrilleAsnAla	1688
QY	1197	AGCTTCTGATGATTTATAGACAGAAAGGCTTACATGCTACACAGGGGCTCTGGCA	1256
DB	1689	SerphelauaspGlyTYrArglnlmglnysalatyrllealatnglnglyProleuAla	1708
QY	1257	GAGAGCACCGAGAGCTTCTGGGCGATGCTATGGAGACAAATCCACCATCATGCTATG	1316
DB	1709	GlnserthnGlnaephethrphargmetLeutrglnhlsansenThrlleleValMet	1728
QY	1317	CTGACCAAGCTTGGGAGATGGGCAAGGAAATGCCACAGTACTGGCCAGCAGAGCGC	1376
DB	1729	LeuthrlyLeuargGlnMetGlyArglnlyscysHslglnlyTYrProleaglAarg	1748
QY	1377	TGTGTCCTGCTACAGACTTGTGTGACCGGATGGCTGATCAACATGCGCCAGTAT	1436
DB	1749	SerAlaArgTYrGlnlyrPheValValaAspProMetAlaGlnlyrAsnMetProGlnTYr	1768
QY	1437	ATCTGCGTGAAGTTCAAGGTACGAGATGCCCGGAGATGGGCACTCAAGCAATCCGCGAG	1496
DB	1769	lleuargGlnPhelelyValThrAspAlaArgaAspGlyGlnSeraerpyrilleArgGln	1788
QY	1497	TTCCCACTTACAGACTGGGCGAGAGAGGCGGCGCCCAAGAGACAGGAGGAGATTCAATGAC	1556
DB	1789	PheGlnPheThrAspTYrProGlnGlnlyValProlysthnGlyGlnGlyPheleleAsp	1808

RESULT 9

Q90YJ5 PRELIMINARY; PRT; 508 AA.

AC Q90YJ5; 091BAS; 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Receptor protein-tyrosine phosphatase IAR (Fragment).
GN PTPR2A OR IAR.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA van der Sar A., Beist M., de Fockert J., Overvoorde J., Zivkovic D., den Hertog J.;

RT "Expression of receptor protein-tyrosine phosphatase alpha, sigma and
IAR during development of the zebrafish embryo."
Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL; AJ111885; CAC44758.1; -
DR ZFIN; ZDB-GENE-020107-2; ptpf.
DR GO; GO:0016787; P:hydrolyase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:000470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; FRTYPEPHTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS50833; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolyase.
FT NON TER

SQ SEQUENCE 508 AA; 58463 MW; 72A6DD348830C446 CRC64;

Alignment Scores:

Pred. No.:	4,796-129	Length:	508
Score:	135.00	Matches:	135
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	11.86%	Indels:	0
DB:	13	Gaps:	0

US-09-719-272-1 (1-3467) x Q90YJ5 (1-508)

QY	1311	GTGATGCTGACCAAGCTTGGGAGATGGGCAAGGAAATGCCACAGTACTGGCGACGA	1370
DB	337	ValMetLeuthrlyleuargGlnMetGlyArglnlyscysHslglnlyTYrProleAla	356
QY	1371	GAGCGCTCTGCTGCTACCAAGTCTTGTGTGACCCGATGGCTGATGACAAATGGCC	1430
DB	357	GluArgSerAlaArgTYrGlnlyrPheValValaAspProMetAlaGlnlyrAsnMetPro	376
QY	1431	CAGTATATCTCGGTGATGTTCAAGGTACAGATGCCCGGATGGGCACTGACGAATC	1490
DB	377	GlnTYrilleuargGlnPhelelyValThrAspAlaArgaAspGlyGlnSeraerpyrille	396
QY	1491	CGGCACTTCAAGTTCAAGACTGCGCCAGAGCGGGCTGCCCAAGACAGGCGAGATTC	1550
DB	397	ArgGlnPheGlnPheThrAspTYrProGlnGlnlyValProlysthnGlyGlnGlyPhe	416
QY	1551	ATTGACTTCAATGGGCGAGGTGATAGACCAAGAGACAGTGTGACAGGATGGGCTATC	1610
DB	417	lleaspPhelelelyValValaHslglnlyrGlnGlnPheGlyGlnAspGlyProle	436
QY	1611	ACGGTGCACTGAGTCTGGCGTGGCGCCAGCCGGGGTGTTCATCACTTGAGCATCGTC	1670
DB	437	ThrValHiscysSerAlaGlyValGlyArglnGlyValPheleleThrleuSerleleVal	456
QY	1671	CTGAGAGCGCATGGGCTATGAGGGCGGTGTCAGATTTCAAGACC	1715
DB	457	LeuGluArgMetArgTYrGlnGlyValValaAspMetPheGlnThr	477

RESULT 10

Q91BAS PRELIMINARY; PRT; 468 AA.

AC Q91BAS; 091BAS; 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RYPTPR2A protein (Fragment).
GN RYPTPR2A.
OS Potamotrygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hymnosqualeae; Pristionorae; Batoidae;
OC Myliobatiformes; Myliobatoidae; Potamotrygonidae; Potamotrygon.
OX NCBI_TaxID=86373;
RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=20219325; PubMed=10754074;
 RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
 RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
 RT divergence of tissue-specific isoform genes in the early evolution of
 RT vertebrates";
 RL J. Mol. Evol. 50:302-311(2000).
 DR EMBL; AB033581; BAA5188.1; -.
 DR HSSP; P18052; LYPO.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHPTAS.
 DR SMART; SM00194; PTPc; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS00386; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_FTP; 2.
 KM Hydrolyase.
 FT NON_TER
 SQ SEQUENCE 468 AA; 53862 MW; 0051F5E0DD7A580 CRC64;

Alignment Scores:
 Pred. No.: 3 42e-99 Length: 468
 Score: 106.00 Matches: 106
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 9.31% Indels: 0
 DB: 13 Gaps: 0

US-09-719-272-1 (1-3467) x Q9TBA5 (1-468)
 QY 1509 GACTGGCCAGAGAGAGCGCGTCCCAAGAGAGCGAGGATTTGACTTACCTGCGGAG 1568
 DB 363 AAPTTPProGluGlnGlnValProlystrGlyGluGlyPheIIAspPheIIeGlyGln 382
 QY 1569 GTGCATPAGACCAAGAGAGAGTTTGACAGATGGGCGCATACAGCGTGCATGCGAGTCT 1628
 DB 383 ValHisIlyThrIlyGlnGlnPheGlyGlnAspGlyProIIeThrValHisGlySerIIa 402
 QY 1629 GCGGTGGCGCGAGCGGGGTGTTCATCTGAGCATGTCTGAGGCGATGCGCTAT 1688
 DB 403 GlyValGlyAryThrGlyValPheIIeThrIleuSerIIeValIleGluIlyrGlySerAryThr 422
 QY 1689 GAGGGGCGGTGCATGTTTTCAGACCGGAGAGACCGCGTACAGAGCGGTCTGCGCATG 1748
 DB 423 GluGlyValValAspMetPheGlnThrValIlyThrIleuAryThrGlnIlyProIIaMet 442
 QY 1749 GTGCAGACAGAGAGACCATATACGCTGTGCTACCGTGGCGCGCTGAGTACCTCGGAGC 1808
 DB 443 ValGlnThrGluAspGlnIlyrGlnIleuGlyAryGlyAlaIleGluIlyrIleuGlySer 462
 QY 1809 TTTGACCATATGCAAGC 1826
 DB 463 PheAspHisIlyrIleuThr 468

RESULT 11
 Q62990 PRELIMINARY; PRT; 140 AA.
 AC Q62990;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Protein tyrosine phosphatase delta (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar Kyoto;

RA Borges I.G., Bowen-Pope D.F.;
 RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U57502; AAB02007.1; -.
 DR HSSP; O06124; 2SHP.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTYPHPTAS.
 DR SMART; SM00194; PTPc; 1.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_FTP; 1.
 FT NON_TER
 SQ SEQUENCE 140 AA; 16525 MW; F1912EF20B2582D7 CRC64;

Alignment Scores:
 Pred. No.: 9.57e-51 Length: 140
 Score: 59.00 Matches: 59
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.18% Indels: 0
 DB: 11 Gaps: 0

US-09-719-272-1 (1-3467) x Q62990 (1-140)
 QY 1311 GTGATGCTGACCAAGCTTGGGAGATGGGAGAGAGAAATGCAACAGTATGCGCAGCA 1370
 DB 39 ValMetIleuThrIlySerIleuGluMetGlyAryGluIlyCysHisGlnIlyrIlyProIIa 58
 QY 1371 GAGCGCTCTGCTGCTGCTACCATGTTGTTGTTGACCCGATGGCTGAGTACACATGCC 1430
 DB 59 GluArySerIIaAryThrGlnIlyrPheValIleAspProMetAlaGluIlyrAsnMetPro 78
 QY 1431 CAGTATATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1487
 DB 79 GlnIlyrIleuAryGluIlyrPheIlyValIleAspAlaAryGlyGlnSerAryThr 97

RESULT 12
 Q8C922 PRELIMINARY; PRT; 192 AA.
 ID Q8C922;
 AC Q8C922;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Unknown EST (Fragment).
 DB Unknwnn EST (Fragment).
 GN PTPRD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 DR EMBL; AK043201; BAC31488.1; -.
 DR MGD; MGI:97812; Ptpyd.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003595; PTPc_motif.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTYPHPTAS.
 DR SMART; SM00404; PTPc_motif; 1.
 DR SMART; SM00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS00386; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_FTP; 1.

FT NON TER 1 1
SQ SEQUENCE 192 AA; 22551 MW; B78B194500F33B1A CRC64;
Alignment Scores:
Pred. No.: 9.18e-51 Length: 192
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 11 Gaps: 0
US-09-719-272-1 (1-3467) x Q8C922 (1-192)
QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGCAGGAGAAATGCCACCACTACTGCGCCAGCA 1370
Db 21 ValmetLeuthrLysLeuArgLysGluMetGlyArgGluLysCysHsGlnTyrtPProAla 40
QY 1371 GAGGCGCTGCTGCTGCTACCACTACTTTGTTGTTACCCGATGGCTGAGTACAAATGCC 1430
Db 41 GlutArgSerAlaArgTyrgLntyrPheValValAspProMetAlaGlnTyraAsmMetPro 60
QY 1431 CAGTATATCTGCGCTGAGTTCAAGGTACCGGATGCCCGGATGGCAGTCAAGAGACA 1487
Db 61 GlnTyrtLeuLeuArgLysGluPheValThrAspAlaArgAspGlyGlnSerArgThr 79
RESULT 13
Q62604 PRELIMINARY; PRT; 398 AA.
AC Q62604;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN CPrp1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STAIN=Sprague Dawley; TISSUE=Occipital cortex;
RX MEDLINE=94045925; PubMed=8229209;
RA Sahin M., Hockfield S.;
RT "Protein tyrosine phosphatases expressed in the developing rat
brain.";
RL J. Neurosci. 13:4968-4978(1993).
DR EMBL; U03273; AAC52124.1; -.
DR PIR; I56540; I56540.
DR HSP; F18052; LYFO.
DR GO; GO:0016787; P:hydrolyase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KM Hypothetical protein; Hydrolyase.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 398 AA; 45618 MW; AYCAB3AE6D589E17 CRC64;
Alignment Scores:
Pred. No.: 8.34e-51 Length: 398
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 11 Gaps: 0

US-09-719-272-1 (1-3467) x Q62604 (1-398)
QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGCAGGAGAAATGCCACCACTACTGCGCCAGCA 1370
Db 297 ValmetLeuthrLysLeuArgLysGluMetGlyArgGluLysCysHsGlnTyrtPProAla 316
QY 1371 GAGGCGCTGCTGCTGCTACCACTACTTTGTTGTTACCCGATGGCTGAGTACAAATGCC 1430
Db 317 GlutArgSerAlaArgTyrgLntyrPheValValAspProMetAlaGlnTyraAsmMetPro 336
QY 1431 CAGTATATCTGCGCTGAGTTCAAGGTACCGGATGCCCGGATGGCAGTCAAGAGACA 1487
Db 337 GlnTyrtLeuLeuArgLysGluPheValThrAspAlaArgAspGlyGlnSerArgThr 355
RESULT 14
Q91BA2 PRELIMINARY; PRT; 468 AA.
AC Q91BA2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE RYPR2AB protein (Fragment).
GN RYPR2AB.
OS Potamotrygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hypnosquales; Fisticorales; Batoidae;
OC Myliobatiformes; Myliobatoidae; Potamotrygonidae; Potamotrygon.
OX NCBI_TaxID=86373;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219325; PubMed=10754074;
RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
RT divergence of tissue-specific isoform genes in the early evolution of
vertebrates.";
RL J. Mol. Evol. 50:302-311(2000).
DR EMBL; AB033584; BAA35191.1; -.
DR HSP; F18052; LYFO.
DR GO; GO:0016787; P:hydrolyase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KM Hydrolyase.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 468 AA; 53885 MW; 8B1CAB0E8E969284 CRC64;
Alignment Scores:
Pred. No.: 8.16e-51 Length: 468
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 13 Gaps: 0
US-09-719-272-1 (1-3467) x Q91BA2 (1-468)
QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGCAGGAGAAATGCCACCACTACTGCGCCAGCA 1370
Db 297 ValmetLeuthrLysLeuArgLysGluMetGlyArgGluLysCysHsGlnTyrtPProAla 316
QY 1371 GAGGCGCTGCTGCTGCTACCACTACTTTGTTGTTACCCGATGGCTGAGTACAAATGCC 1430
Db 317 GlutArgSerAlaArgTyrgLntyrPheValValAspProMetAlaGlnTyraAsmMetPro 336
QY 1431 CAGTATATCTGCGCTGAGTTCAAGGTACCGGATGCCCGGATGGCAGTCAAGAGACA 1487

Db 337 GlnTyrlleuArgGluPheIysValThrAspAlaArgAspGlyGlnSerArgThr 355

RESULT 15

Q91BA0 PRELIMINARY; PRT; 468 AA.

AC Q91BA0; 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE RYPTPR2AC protein (Fragment).
 GN RYPTPR2AC
 OS Potamotrygon motoro (South American freshwater stingray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalia; Hynostomata; Pristigasteridae; Batoidae;
 OC Myliobatiformes; Myliobatoidae; Potamotrygonidae; Potamotrygon.
 OX NCBI_TaxID=86373;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20219325; PubMed=10754074;
 RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
 RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;
 RT divergence of tissue-specific isoform genes in the early evolution of
 RT vertebrates.";
 RL J. Mol. Evol. 50:302-311(2000).
 DR EMBL; AB033586; BAA95193.1; -.
 DR HSSP; P18052; 1XPO.
 DR GO; GO:0016787; P:hydrolyase activity; IEA.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR002422; TYR_PP.
 DR Pfam; PF0102; Y_phosphatase; 2.
 DR PRINTS; PR00700; _PRTYPHPTASE.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydrolyase.
 KW NON TER
 FT
 SQ SEQUENCE 468 AA; 53976 MW; 76C975D92D437A86 CRC64;

Alignment Scores:

Pred. No.:	8.16e-51	Length:	468
Score:	59.00	Matches:	59
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.18%	Indels:	0
DB:	13	Gaps:	0

US-09-719-272-1 (1-3467) x Q91BA0 (1-468)

QY	1311	GTCATGCTGACCAAGCTTCGGAGATGGGACAGAGAAATGCCACCACTGAGCCACGA	1370
Db	297	ValMetLeuThrIleuArgGluMetGlyArgGluIysCysHISGlnTyrlTrpProAla	316
QY	1371	GAGCGCTGCTGCTGCTACCAAGTACTTTGTTGTTGACCCGATGGCTGAGTCAACATGCC	1430
Db	317	GluArgSerAlaArgIleGlnTyrlPheValValAspProMetCAlaGlnTyrlAsnMetPro	336
QY	1431	CAGTATATCTGCGGTGAGTTCAAGTCAAGATGCCCGGATGGCAGTCAAGACGA	1487
Db	337	GlnTyrlIleuArgGluPheIysValThrAspAlaArgAspGlyGlnSerArgThr	355

Search completed: March 9, 2004, 09:10:14
 Job time : 207 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 9, 2004, 08:56:28 ; Search time 55 Seconds
(without alignments)
12127.126 Million cell updates/sec

Title: US-09-719-272-1

Perfect score: 1138
Sequence: 1 gatccgacgaagactcc.....attgataatcagattctt 3467

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Word size: 1

Total number of hits satisfying chosen parameters: 565818

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-Q=/cgn2/USPRO.spool/p/US09719272/runat.09032004.085230.7466/app.query.fasta.1.3655
-DB=PIR_78 -QFWT=fastan -SUFFIX=xlp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=01390 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc
-NORExt -HEA=SITE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09719272.QCGN.1.1.87@runat.09032004.085230.7466 -NCPU=6 -ICPU=3
-NO MMAP -LARGESUBSTRY -NEG SCORES=0 -WAIT -DSBLOC=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6
-Fgapext=7 -YGAPOP=60 -YGAPEXT=60 -DELop=6 -DELExt=7

Database :

1: PIR_78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	607	53.3	1897	1 TDRHUK
2	259	22.8	1290	2 A56493
3	254	22.3	1898	2 A56216
4	250	22.0	582	2 A47068
5	108	9.5	108	2 S40292
6	59	5.2	398	2 I56540
7	59	5.2	1499	2 I50212
8	59	5.2	1501	2 I58148
9	59	5.2	1863	2 S46217
10	59	5.2	1907	2 S50893
11	59	5.2	1912	2 A56178
12	54	4.7	1691	1 D54689
13	54	4.7	1894	1 C54689
14	46	4.0	1231	2 S53089

15	40	3.5	1437	2 T31093	probable protein-t
16	35	1.496	1	A48758	protein-tyrosine-p
17	34	3.0	2029	1 TDPFHK	protein-tyrosine-p
18	25	2.2	2051	1 T30938	receptor tyrosine
19	23	2.0	1262	1 B48758	protein-tyrosine-p
20	14	1.2	2302	2 T14328	protein-tyrosine-p
21	13	1.1	88	2 A44929	protein-tyrosine-p
22	13	1.1	106	2 S40282	protein-tyrosine-p
23	12	1.1	198	2 T27722	hypothetical prote
24	12	1.1	256	2 A40169	protein-tyrosine-p
25	12	1.1	483	2 T25992	hypothetical prote
26	12	1.1	521	1 A44267	protein-tyrosine-p
27	12	1.1	583	2 S17671	protein-tyrosine-p
28	12	1.1	699	2 C6132	protein-tyrosine-p
29	12	1.1	700	1 S12053	protein-tyrosine-p
30	12	1.1	796	1 J12185	protein-tyrosine-p
31	12	1.1	802	1 A36065	protein-tyrosine-p
32	12	1.1	829	1 A47373	protein-tyrosine-p
33	12	1.1	1174	2 I18140	protein-tyrosine-p
34	12	1.1	1175	2 S51005	protein-tyrosine-p
35	12	1.1	1176	2 I58345	protein-tyrosine-p
36	12	1.1	1187	1 J14155	protein-tyrosine-p
37	12	1.1	1189	1 J14155	protein-tyrosine-p
38	12	1.1	1200	2 T43148	probable protein-t
39	12	1.1	1237	2 A54080	protein-tyrosine-p
40	12	1.1	1273	1 TDRHUK	leukocyte common a
41	12	1.1	1291	1 A28334	protein-tyrosine-p
42	12	1.1	1301	1 A41622	protein-tyrosine-p
43	12	1.1	1304	1 A46546	leukocyte common a
44	12	1.1	1422	2 T42636	protein-tyrosine-p
45	12	1.1	1440	2 J16312	protein-tyrosine-p

ALIGNMENTS

RESULT 1
TDRHUK
leukocyte antigen-related protein precursor - human
N/Alternate names: leukocyte common antigen homolog
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 22-Jun-1999
C/Accession: S03841, J10051
R/Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 169, 1523-1530, 1988
A/Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region
A/Reference number: J10051; MIM:8903578; PMID:2972792
A/Residues: 1-1897 <SP>
A/Status: nucleic acid sequence not shown
A/Accession: S03841
A/Molecule type: mRNA
A/Cross-references: EMBL:Y00815; NID:G34266; PDB:CA68754.1; PID:G34267
C/Genetics:
A/Gene: GDB:FTPRF, LAR
A/Cross-references: GDB:120138; OMIM:179590
A/Map position: 1p34-1p34
C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog
C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
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F/17-1250/Domain: extracellular #status: predicted <EXT>
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F/139-199/Domain: immunoglobulin homology <IMM2>
F/236-290/Domain: immunoglobulin homology <IMM3>
F/308-390/Domain: fibronectin type III repeat homology <FN3A>
F/403-489/Domain: fibronectin type III repeat homology <FN3B>
F/501-583/Domain: fibronectin type III repeat homology <FN3C>
F/596-685/Domain: fibronectin type III repeat homology <FN3D>
F/698-798/Domain: fibronectin type III repeat homology <FN3E>
F/810-893/Domain: fibronectin type III repeat homology <FN3F>
F/905-989/Domain: fibronectin type III repeat homology <FN3G>
F/1001-1078/Domain: fibronectin type III repeat homology <FN3H>

F:1251-1274/Domain: transmembrane #status predicted <TM>
 F:1275-1897/Domain: intracellular #status predicted <INT>
 F:1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LCA>
 F:1365-1886/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F:44-97/146-197,243-268/Disulfide bonds: #status predicted
 F:107,240,268,711,956/Binding site: carbonyl (Asn) (covalent) #status predicted
 F:1538/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1544/Binding site: substrate phosphate (Arg) #status predicted
 F:1826/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1835/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Mismatches:	Best Local Similarity:	Query Match:
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100.00%					0		
53.34%					0		
					0		

US-09-719-272-1 (1-3467) x TDHUK (1-1897)

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QY 6 GGAAGTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 65
DB 1291 GATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1310
QY 66 TACCAAGACCCAGGTATGCGAGACCAACCCCACTCCCATCCAGACCTGGCGGACAAAC 125
DB 1311 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1330
QY 126 ATGAGAGCGCTCAAGACCAACGATGGCTCAAGTCTCCAGAGATGAGAGCTCAAC 185
DB 1331 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1350
QY 186 CCTGAGACAGAGTTCAGTGGAGAAATTCAACTGAGAGTGAACAAGCCCAAGACCGC 245
DB 1351 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1370
QY 246 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 305
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QY 306 CCGGAGAGTACTACATCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 365
DB 1391 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1410
QY 366 ATGCGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 425
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QY 426 CAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 485
DB 1431 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1450
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DB 1451 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1470
QY 546 GATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 605
DB 1471 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1490
QY 606 AGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 665
DB 1491 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1510
QY 666 GATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 725
DB 1511 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1530
QY 726 GATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 785
DB 1531 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1550

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QY 786 ATGATGCAATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 845
DB 1551 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1570
QY 846 ACCGTGATGCAATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 905
DB 1571 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1590
QY 906 CATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 965
DB 1591 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1610
QY 966 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1025
DB 1611 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1630
QY 1026 CTGAGATGCAATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1085
DB 1631 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1650
QY 1086 CTGCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1145
DB 1651 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1670
QY 1146 GTGCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1205
DB 1671 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1690
QY 1206 GATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1265
DB 1691 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1710
QY 1266 GATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1325
DB 1711 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1730
QY 1711 GATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1730
DB 1731 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1750
QY 1326 CTGCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1385
DB 1751 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1770
QY 1386 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1445
DB 1771 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1790
QY 1446 GATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1505
DB 1791 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1810
QY 1506 ACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1565
DB 1811 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1830
QY 1566 CAGGATGCAATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1625
DB 1831 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1850
QY 1626 GATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1685
DB 1851 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1870
QY 1686 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1745
DB 1871 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1860
QY 1746 ATGCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1805
DB 1891 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1920
QY 1806 AGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1826
DB 1891 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1950
QY 1871 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1890
DB 1951 TATGCTAAAGACCTCTGTTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 1970

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F/149-209/Domains: immunoglobulin homology <IMM2>
 F/246-309/Domains: immunoglobulin homology <IMM3>
 F/318-400/Domains: fibronectin type III repeat homology <FN3A>
 F/413-499/Domains: fibronectin type III repeat homology <FN3B>
 F/511-593/Domains: fibronectin type III repeat homology <FN3C>
 F/606-695/Domains: fibronectin type III repeat homology <FN3D>
 F/708-799/Domains: fibronectin type III repeat homology <FN3E>
 F/811-895/Domains: fibronectin type III repeat homology <FN3F>
 F/906-990/Domains: fibronectin type III repeat homology <FN3G>
 F/1003-1079/Domains: fibronectin type III repeat homology <FN3H>
 F/1282-1375/Domains: (or 1259-1275) transmembrane #status predicted <TM>
 F/1276-1898/Domains: intracellular #status predicted <INT>
 F/1286-1898/Domains: leukocyte common antigen cytosolic domain homology <LAC>
 F/1366-1887/Domains: protein-tyrosine-phosphatase homology <PTP1>
 F/1655-1878/Domains: protein-tyrosine-phosphatase homology <PTP2>
 F/54-107,156-207,253-298/Dissulfide bonds: #status predicted
 F/117-250,295,721,957/Binding site: carbohydrate (Aan) (covalent) #status predicted
 F/153/Active site: Cys (phosphocysteine intermediate) #status predicted
 F/1545/Binding site: substrate phosphate (Arg) #status predicted
 F/1830/Active site: Cys (phosphocysteine intermediate) #status predicted
 F/1836/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:
 Pred. No.: 1.6e-211 Length: 1898
 Score: 254.00 Matches: 254
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 22.32% Indels: 0
 DB: 2 Gaps: 0
 US-09-719-272-1 (1-3467) x S46216 (1-1898)

QY 1065 TCCCGCTTCATCAGCCGCCCACTGCCCTTCACCAAGTTCAGAACCGCGTGTACATC 1124
 DB 1645 SerArgPheIleSerIleAsnLeuProCysAsnLysPheLysAsnArgLeuValAsnIle 1664
 QY 1125 ATCCCTACGAATTGACCCCGTGTGTCTGCAGCCCATCCGTGTGTGGAGGCTCTGAC 1184
 DB 1665 MetProTyrGluLeuThrArgValCysLeuGlnProIleArgGlyValGlnLysSerAsp 1684
 QY 1185 TACATCAATGCCAGCTTCTCGATGTTTAAACAGACAGAAAGCCCTACATAGCTACAG 1244
 DB 1685 TyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGln 1704
 QY 1245 GGGCGCTGTGACAGAGACAGACCGAGACTCTGGCGCATCTATGGAGACCAATTCACC 1304
 DB 1705 GlyProLeuAlaGluSerThrGlnLysPheThrPargMetLeuTrpGlnHisSerThr 1724
 QY 1305 ATCATGTGATGCTGACCAAGCTTGGAGAGATGGGAGAGAAATGCCACCAATCTGG 1364
 DB 1725 IleIleValMetLeuThrLysLeuArgGlnMetGlyArgGlnLysCysHisGlnTyrTrp 1744
 QY 1365 CGAGCAGAGCGCTGTGTGCTACAGTACTTGTGTGTGACCCGATGGCTGATGATCAAC 1424
 DB 1745 ProIleGlnArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGlnLysTran 1764
 QY 1425 ATGCCCAATATTCCTGCGTGAATTCAGCTCAAGATGCCCGGAGATGGCGATCAAG 1484
 DB 1765 MetProGlnTyrIleLeuArgGlnPheLysValThrAspAlaArgAspGlyGlnSerArg 1784
 QY 1485 ACAATCGGAGATTCAGTTCAGACTGAGCAGAGAGAGGCGCTGCCAAGACAGCGAG 1544
 DB 1785 ThrIleArgGlnPheGlnPheMetPargProGlnGlnLysAlaProLysThrGlnGln 1804
 QY 1545 GAGATTCATGATTCATCGGCGAGAGTGCATTAAGACCAAGAGCAAGTTTGACAGATGG 1604
 DB 1805 GlyPheIleAspPheIleGlyGlnValIleLysThrLysGlnGlnPheGlyGlnAspGly 1824
 QY 1605 CCATTCAGGATGCTGAGTGCAGTGGCGAGCGAGCGAGGAGTTCATCACTGAC 1664
 DB 1825 ProIleThrValHisCysSerAlaGlyValGlyArgThrGlyValPheIleThrLysSer 1844
 QY 1665 ATGCTCTGAGCGCAGCATGCGCTATGAGGCGGTGTGCACATGTTTCAGACCGTGAAC 1724

DB 1845 IleValLeuGlnArgMetArgTyrGlnLysValValAlaPheMetPheGlnThrValLysThr 1864
 QY 1725 CTGCGACACAGCGCTCTGCATGATGTCAGACAGACAGACAGATCACTGCTACCGT 1784
 DB 1865 LeuArgThrGlnArgProAlaMetValGlnThrGlnLysArgGlnLysCysTyrArg 1884
 QY 1785 GGGCGCTGTGAGTACTCTGGCGAGCTTGTGACCACTATGCAAG 1826
 DB 1885 AlaAlaLeuGlnTyrLeuGlnSerPheAspHisTyrAlaThr 1898

RESULT 4

A57068
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)
 N/A/Alternate names: leukocyte antigen-related protein LAR
 C/Species: Mus musculus (house mouse)
 C/Date: 03-Oct-1995 #sequence_revision 09-Mar-1996 #text_change 23-Jul-1995
 C/Accession: A57068, S40280
 R/Schaepeveld, R.Q.J., van den Maagdberg, A.M.J.M., Schepens, J.T.G., Olde Weghuis, Genomics 27, 124-130, 1995
 A/Title: The mouse gene pPrf encoding the leukocyte common antigen-related molecule
 A/Reference number: A57068; MID:95394448; PMID:7665159
 A/Accession: A57068
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-582 <SCH>
 A/Cross-references: GB:237988; NID:993005; PIDN:CAA8070.1; PID:993006
 R/Hendriks, W.; Bruma, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
 A/Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
 A/Accession: S40280
 A/Reference number: S40280
 A/Molecule type: mRNA
 A/Residues: 116-221 <HEN>
 A/Cross-references: EMBL:Z23049; NID:9438135; PIDN:CAA80584.1; PID:9438136
 A/Genetic: PUPRF
 C/Suprafamily: leukocyte antigen-related protein, fibronectin type III repeat homology
 C/KeyWords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembr
 F/1-582/Domains: leukocyte common antigen cytosolic domain homology (fragment) <LAC>
 F/150-221/Domains: protein-tyrosine-phosphatase homology <PTP2>
 F/338-562/Domains: protein-tyrosine-phosphatase homology <PTP2>
 F/223/Active site: Cys (phosphocysteine intermediate) #status predicted
 F/223/Binding site: substrate phosphate (Arg) #status predicted
 F/514/Active site: Cys (phosphocysteine intermediate) #status predicted
 F/520/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:
 Pred. No.: 6.11e-208 Length: 582
 Score: 250.00 Matches: 250
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 21.97% Indels: 0
 DB: 2 Gaps: 0
 US-09-719-272-1 (1-3467) x A57068 (1-582)

QY 1077 AGCGCCAACTGCGCTTCACCAAGTTCAGAAACCGGCTGTGAAACATGACCCCTACGA 1136
 DB 333 SerIleAsnLeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGln 352
 QY 1137 TTGACCGGTGTGTCTGCAGCCCATCCGTGTGTGAGGCTCTGATCAATCAATGCC 1196
 DB 353 LeuThrArgValCysLeuGlnProIleArgGlyValGlnLysSerAspTyrIleAsnAla 372
 QY 1197 AGCTTCTGATGTTTAAACAGACAGAAAGCCCTACATCAAGGCGCTCGGCA 1256
 DB 373 SerPheLeuAspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnLysProLeuAla 392
 QY 1257 GAGAGACCGAGACTCTGGCGCATCTATGGAGACCAATTCACCATCATGTCATG 1316
 DB 393 GluSerThrGlnLysPheThrPargMetLeuTrpGlnHisSerThrIleIleValMet 412

QY 1317 CTACCAAGGCTTCGGGGAGATGGGACAGGAGAAATGCAACAGATACGCGACAGAGAGCCG 1376

Db 413 LeuThrIlyLeuArgIuMetGlyArgGluIlyCysHisGlnIlyTrpProIlaGluArg 432

QY 1377 TCTGCTGGCTACCAAGTACTTTGTGTGTGACCCGAGCTGAGTACCAATGCCCGAT 1436

Db 433 SerAlaArgIyGlnIyPheValIValAspPheMetIaGluIyTrpAsnMetProGlnIy 452

QY 1437 ATCCTGGGAGTTTCAAGGTCACGGATGCCCGGATGGGAGTCAAGAGCAATCCGGCAG 1496

Db 453 IleuArgIuPheIyValIlnAspAlaArgGlnIyGlnSerArgTrIleArgIln 472

QY 1497 TTCAGTTTCAAGACTGGCCAGAGACAGGGCGTGCCCAAGACAGCCAGGGATTCATTGAC 1556

Db 473 PheGlnPheThrAspTrpProGluGlnIyValProIyThrGluIyGluPheIleAsp 492

QY 1557 TTCATCGGCGAGGTCGCTAATAAGCCAAAGAGACAGTTTGAAGAGATGGGCGCTATACGGT 1616

Db 493 PheIleGluIlnValAlaIlySerIlnIyGluIlnPheIyGlnIlnAspGlyProIleIlnVal 512

QY 1617 CACTGCAGTGTGGCGTGGCGCCAGCCGGGGTGTTCATCACTGTAGCATGTCTGGAG 1676

Db 513 HisCysSerIlaGluIyValGlyArgThrGlyValPheIleThrIleuSerIleValIleGlu 532

QY 1677 CGCATGGCGCTATGAGGGCGCTGGTGCATGTTTCAAGCCGCTGAAGACCCGCGCTACACAG 1736

Db 533 ArgPheIaArgIyGluIyValIValAspMetPheGlnIlnThrValIlySerIleuArgIlnGln 552

QY 1737 CGATCGTCAGTGTGCAGACAGAGACAGACAGTATGAGTGTGTCTACCGTGGCGGCTGGAG 1796

Db 553 ArgProIaMetValGlnIlnThrGluAspGlnIyGlnIleuSerIyArgIaIaIeGlu 572

QY 1797 TACTTCGGCAGCTTTGACCACTATGCAACG 1826

Db 573 TyrIleuGlySerPheAspHisTyrAlaThr 582

RESULT 5

S40292

C Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)

C Species: Mus musculus (house mouse)

C Date: 06-Mar-1994 #sequence_revision 15-Mar-1996 #text_change 23-Mar-2001

C Accession: S40292

R Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.

A Submitted to the EMBL Data Library, June 1993

A Description: Assessment of the expression levels of murine protein-tyrosine phosphatases

A Reference number: S40280

A Accession: S40292

A Status: Preliminary

A Molecule type: mRNA

A Residues: 1-108 <EMBL>

A Cross-references: KMBL:Z23061, NID:G438159, PIDN:CA080596.1; PID:G438160

C Superfamily: leukocyte antigen-related protein, fibronectin type III repeat homology, C/

C Keywords: glycoprotein, phosphoric monoester hydrolase; transmembrane protein; tyrosinase

F1-108/Domain: leukocyte common antigen cytosolic domain homology (fragment) <LAC>

Alignment Scores:

Paid. No.:	9,54e-85	Length:	108
Score:	108.00	Matches:	108
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.49%	Indels:	0
DB:	2	Gaps:	0

US-09-719-272-1 (1-3467) x S40292 (1-108)

QY 1293 CACAATTCACCATCATGTCATGCTGACCAAGCTTCGGAGATGGCGAGAGAGAAATGC 1352

Db 1 HisAsnSerThrIleIleValMetLeuThrIlyLeuArgGluMetGlyArgGluIyCys 20

QY 1353 CACCGTACTGGCCAGACAGAGCGCTCTGCTCGCTACCAAGTACTTTGTGTGTGAACCCGATG 1412

Db 21 HisGlnTyrTrpProAlaGluArgSerAlaArgTyrGlnTyrPheValValAspProMet 40

QY 1413 GTTGAGTACCAACATGCCCCAGTATATCTTCGCGTGAAGTTCAGAGTCACGGATGCCCGGAT 1472

Db 41 AlAGlulTyrAsnMetProGlnTyrIleLeuArgGluPheValThrAspAlaArgAsp 60

QY 1473 GGGCAGTCAAGAGCAATCCGGGAGTTCAGGTTCCAGTTCACAGACTGGCCAGAGCGGCGGCC 1532

Db 61 GlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGlnGlnValPro 80

QY 1533 AAGACAGCGAGGAGGATTCATTGACTTCATTCGGGAGGTGCAATAAGACCAAGAGCACTTT 1592

Db 81 LysThrGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThrLysGlnGlnPhe 100

QY 1593 GGACAGGATGGGCGCTATCAAGGTG 1616

Db 101 GlyGlnAspGlyProIleThrVal 108

RESULT 6

156540
protein-tyrosine-phosphatase (EC 3.1.3.48) ctp1 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 26-Jul-1996 #sequence _revision 26-Jul-1996 #text_change 23-Jul-1999

C:Accession: 156540

R:Salini, M.; Hockfield, S.

J. Neurosci. 13, 4966-4978, 1993

A:Title: Protein tyrosine phosphatases expressed in the developing rat brain.

A:Reference number: 156540; MUID:94045925; PMID:8229209

A:Accession: 156540

A>Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-398 <RMS>

A:Cross-references: EMBL:U03273; NID:9414996; PIDN:AAC52124.1; PID:9414997

C:Genetics:

A:Gene: ctp1

C:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homolc

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosph

P/1-157/Domain: protein-tyrosine-phosphatase homology (fragment) <PRP>

P/225-398/Domain: protein-tyrosine-phosphatase homology (fragment) <PRP>

P/109/Active site: Cys (phosphocysteine intermediate) #status predicted

P/115/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:

Pred. No.:	2.02e-42	Length:	398
Score:	59.00	Matches:	59
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.18%	Indels:	0
DB:	2	Gaps:	0

US-09-719-272-1 (1-3467) x 156540 (1-398)

QY 1311 GTCATGCTACCAAGCTTCGGGAGATGGGCGAGGAATTCACCACTACTGCGCACGA 1370

Db 297 ValMetLeuThrIlySLeuArgGluMetCylArgGlyLysCysHisGlnTyrTrpProAla 316

QY 1371 GAGGCGCTGCTGCGGTACCACTACTTGTATTGTAACCGAGTGGCGTGAACAATGCC 1430

Db 317 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGlnTyrAsnMetPro 336

QY 1431 CAGTATATCTGCGGTGACTTCAGGTCACGAGTCCCGGAGTGGGCACTCAAGACA 1487

Db 337 GlnTyrIleLeuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArgThr 355

RESULT 7

150212
protein-tyrosine-phosphatase (EC 3.1.3.48) chicken

C:Species: Gallus gallus (chicken)

C>Date: 13-Sep-1996 #sequence _revision 13-Sep-1996 #text_change 21-Jan-2000

C:Accession: 150212

R:Stoker, A.W.

Mech. Dev. 46, 201-217, 1994

Alignment Scores:	
Pred. No.:	1.49e-42
Score:	59.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	5.18%
DB:	2
Length:	1499
Matches:	59
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

RESULT B
I58148

C:\Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000
C:\Accession: I58148; S46218
R:\Walton, K.M.; Marcell, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.

A/Accession: I58148
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Description: 11701 bp

A;Title: Molecular cloning and expression of a unique
A;Reference number: S46216; MUID:94347119; PMID:80680212
A;Accession: S46218

A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-1501 <ZHA>
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 103

C1S:superfamily: leukocyte antigen-related protein, fibronectin type III repeat homology; A1C:cross-references: EMBL:U12329; NID:9294573; PIDN:AAC37657.1; PID:9294574; C1S:superfamily: leukocyte antigen-related protein, fibronectin type III repeat homology; 097

C; keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyros

Alignment Scores:	
Pred. No.:	1.49e-42
Score:	59.00
Percent Similarity:	100.00%
Best local Similarity:	100.00%
Query Match:	5.18%
DB:	2
Length:	150
Matches:	59
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

OY

1431 CAGTATTCCTGGGTGAGTTCAAGGTCACCGATGCC
|||||
1370 GATTCTTAATAAATCCTGAATCATGCATCCAAACAAGA

protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat
S4621/
N;Alternate names: leukocyte common antigen-related phosphatase
C:Species: Rattus norvegicus (Norway rat)

C/Species: radicus holvegicus (holvegicus)
C/Date: 07-May-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C/Accession: S46217; S51174; A49104
R: Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.

Biochem. J. 302, 39-47, 1994
A/Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine
A/Reference number: S46216; MUID:94347119; PMID:8068021

A1:Accession: S46217
A1:Status: nucleic acid sequence not shown
A1:Molecule type: mRNA

A/Residues: 1-1863 <ZNA>
A/Cross-references: EMBL:L11587
R/Goldstein, B.J.

submitted to the EMBL Data Library, February 1993
 A/Reference number: S51174
 A/Accession: S51174

A:Molecule type: mRNA
A:Residues: 1-1788, 'G', 1790-1863 <GOL>
A:Cross-references: EMBL:U11587; NID:9205134; PIDN:AAC37656.1; PID:9205135

A/Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the

A/Reference number: A49104; MUID:94043351; PMID:822/050
A/Accession: A49104
A/Status: preliminary; not compared with conceptual translation
A/Remarks: none

A/Molecule type: nucleic acid
A/Residues: 1-596, 'R', 598-603, 'I', 967-1788, 'G', 1790-1863 <YAN>
A/Experimental source: brain
A/Note: Residues extracted from NCBI backbone (NCBIR.139669)

cygword: 31;emmatype: 1;wccorrbeta: 1;phosphorib: 1;phosphoric monoesphaz
A/Note: Sequence extracted from NBLI database (wccorrb: 1;35663)
C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolo

E:160-200/Domain: protein-tyrosine-phosphatase #stratus predicted <MNT>
 F:137-1663/Product: homophilic <MNT>
 C:126/Domain: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester
 #stratus predicted <SIG>

F:149-209/Domain: Immunoglobulin homology <IPI>

F.246-300/Domain: immunoglobulin homology <IMM2>
 F.318-400/Domain: fibronectin type III repeat homology <FN3A>
 F.413-499/Domain: fibronectin type III repeat homology <FN3B>
 F.511-592/Domain: fibronectin type III repeat homology <FN3C>
 F.1244-1863/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F.1331-1552/Domain: protein-tyrosine phosphatase homology <PTP1>
 F.1504/Active site: Cys (phosphocysteine intermediate) #status predicted
 F.1510/Binding site: substrate phosphate (Arg) #status predicted
 F.1795/Active site: Cys (phosphocysteine intermediate) #status predicted
 F.1801/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:

Pred. No.: 1,426-42 Length: 1863
 Score: 59.00 Matches: 59
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.18% Indels: 0
 DB: 2 Gaps: 0

US-09-719-272-1 (1-3467) x S46217 (1-1863)

QY 1311 GTCATGCTGACCAAGCTTGGGAGATGGCGAGAAATGCCACGACTGGCCAGCA 1370
 Db 1692 ValmetLeuThrLysLeuArgGluMetGlyArgGlnLysCysHisGlnTyrrProAla 1711
 QY 1371 GAGCGCTGCTGCTGCTACCAAGTCTTGTGTGACCCGAGTGGCTGAGTCAACATGCC 1430
 Db 1712 GUAAGSerAlaArgTyrrGlnTyrrPheValAlaAspProMetAlaGlnTyrrAsnMetPro 1731
 QY 1431 CAGTATATCTGCTGCTGACTTCAAGGTCCAGATGCCGAGTGGCGAGTCAAGACA 1487
 Db 1732 GlnTyrrLeuArgGluPheValThrAspAlaArgAspGlyGlnSerArgThr 1750

RESULT 10

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
 A/Accession: S50893; S40281
 R/Wagner, J.; Boerboom, D.; Tremblay, M.L.
 Eur. J. Biochem. 226, 773-782, 1994
 A/Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type
 A/Reference number: S50893; MUID:95112841; PMID:7529177
 A/Accession: S50893
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1907 <WAG>
 A/Cross-references: EMBL:X82288; NID:G587483; PIDN:CAA57732.1; PID:G587484
 R/Hendriks, W.; Brugman, C.; Zeeuwen, F.; Schepens, J.; Wieringa, B.
 submitted to the EMBL Data Library, June 1993
 A/Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
 A/Reference number: S40280
 A/Accession: S40281
 A/Molecule type: mRNA
 A/Residues: 1441-1501, 'E', 1503-1546 <HEN>
 A/Cross-references: EMBL:Z23050; NID:G438137; PIDN:CAA0585.1; PID:G438138
 C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy
 C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
 F.149-209/Domain: immunoglobulin homology <IMM1>
 F.246-300/Domain: immunoglobulin homology <IMM2>
 F.413-506/Domain: fibronectin type III repeat homology <3PR>
 F.1128-1907/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F.1137-1596/Domain: protein-tyrosine phosphatase homology <PTP1>
 F.1564-1887/Domain: protein-tyrosine phosphatase homology <PTP2>
 F.1548/Active site: Cys (phosphocysteine intermediate) #status predicted
 F.1554/Binding site: substrate phosphate (Arg) #status predicted
 F.1833/Active site: Cys (phosphocysteine intermediate) #status predicted
 F.1845/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:
 Pred. No.: 1,426-42 Length: 1907
 Score: 59.00 Matches: 59

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.18% Indels: 0
 DB: 2 Gaps: 0

US-09-719-272-1 (1-3467) x S50893 (1-1907)

QY 1311 GTCATGCTGACCAAGCTTGGGAGATGGCGAGAAATGCCACGACTGGCCAGCA 1370
 Db 1736 ValmetLeuThrLysLeuArgGluMetGlyArgGlnLysCysHisGlnTyrrProAla 1755
 QY 1371 GAGCGCTGCTGCTGCTACCAAGTCTTGTGTGACCCGAGTGGCTGAGTCAACATGCC 1430
 Db 1756 GUAAGSerAlaArgTyrrGlnTyrrPheValAlaAspProMetAlaGlnTyrrAsnMetPro 1775
 QY 1431 CAGTATATCTGCTGCTGACTTCAAGGTCCAGATGCCGAGTGGCGAGTCAAGACA 1487
 Db 1776 GlnTyrrLeuArgGluPheValThrAspAlaArgAspGlyGlnSerArgThr 1794

RESULT 11

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human
 N/Alternate names: protein-tyrosine-phosphatase BPT-2
 C/Species: Homo sapiens (man)
 C/Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 21-Jan-2000
 A/Accession: A56178; S12052; B44929
 R/Pullio, R.; Krueger, N.X.; Serra-Pages, C.; Salto, H.; Streuli, M.
 J. Biol. Chem. 270, 6722-6728, 1995
 A/Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.
 A/Reference number: A56178; MUID:95204468; PMID:7896816
 A/Accession: A56178
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1912 <PTU>
 A/Cross-references: GB:IJ38929; NID:G755652; PIDN:AA41749.1; PID:G755653
 R/Krueger, N.X.; Streuli, M.; Salto, H.
 EMBO J. 9, 3241-3252, 1990
 A/Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatase
 A/Reference number: S12049; MUID:9106018; PMID:2170109
 A/Accession: S12052
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 390-1912 <REU>
 A/Cross-references: GB:X54133; NID:G35789; PIDN:CAA8068.1; PID:G35780
 A/Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 56
 R/Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinode, Y.; Imai, K.;
 Cancer Res. 52, 737-740, 1992
 A/Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.
 A/Reference number: A44929; MUID:92119637; PMID:1370651
 A/Accession: B44929
 A/Molecule type: mRNA
 A/Residues: 1756-1804, 'C', 1806-1845 <ADA>
 A/Cross-references: GB:S78086; NID:G243545; PIDN:AA821147.1; PID:G243546
 A/Experimental source: pre-B cell NALM-6
 A/Note: sequence extracted from NCBI backbone (NCBI:78086, NCBI:78087)
 A/Note: the authors did not report the entire codon for residue 90
 C/Genetics:
 A/Gene: GDB:PTPRD
 A/Cross-references: GDB:131384; OMIM:601598
 A/Map position: 9p24-9p24
 C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy
 C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
 F.38-100/Domain: immunoglobulin homology <IMM1>
 F.140-209/Domain: immunoglobulin homology <IMM2>
 F.250-304/Domain: immunoglobulin homology <IMM3>
 F.711-811/Domain: fibronectin type III repeat homology <3PR>
 F.1293-1912/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F.1669-1892/Domain: protein-tyrosine phosphatase homology <PTP2>
 F.1553/Active site: Cys (phosphocysteine intermediate) #status predicted
 F.1559/Binding site: substrate phosphate (Arg) #status predicted
 F.1844/Active site: Cys (phosphocysteine intermediate) #status predicted

SS3089
 protein-tyrosine-phosphatase (EC 3.1.3.48) AnLAR - African malaria mosquito (fragment)
 N:Alternate names: leukocyte antigen-related protein
 C/Species: Anopheles gambiae (African malaria mosquito)
 C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C/Accession: S53089
 R/Spiers, S.
 submitted to the EMBL Data Library, March 1995
 A/Description: Anlar-a transmembrane, receptor-like protein tyrosine phosphatase from th
 A/Reference number: S53089
 A/Accession: S53089
 A/Molecule type: DNA
 A/Residues: 1-1231 <SPI>
 A/Cross-references: EMBL:X85217; NID:G732549; PIDD:CAA59483.1; PIDD:G732550
 C/Genetics:
 A/Introns: 1026/3; 1070/3; 1209/3
 C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology/
 ogy
 C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
 F/208-293/Domain: fibronectin type III repeat homology <3FR>
 F/619-1231/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F/988-1211/Domain: protein-tyrosine-phosphatase homology <PTP>
 F/872/Active site: Cys (phosphocysteine intermediate) #status predicted
 F/1163/Active site: Cys (phosphocysteine intermediate) #status predicted
 F/1169/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:

Pred. No.:	2,866-31	Length:	1231
Score:	46.00	Matches:	46
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	4.04%	Indels:	0
DB:	2	Gaps:	0

US-09-719-272-1 (1-3467) x S53089 (1-1231)

OY 1545 GGATTCATTGACTTATCGGCGAGCGATGATAGACGAGAGAGATTGACAGATGG 1604
 |||||
 DB 1138 GYpHeiLeApHeiLeGlyGlnValHisLeYThrLySGluGlnPheGlyGlnAspGly 1157
 |||||
 OY 1605 CCTATCAGGTCAGTGCAGTGTGCGTGGCGGCGACCGGGGTTCATCATCTGTGAC 1664
 |||||
 DB 1158 ProIeInValHisCysSerAlaGlyValGlyArgThrGlyValPheIleThrLeuSer 1177
 |||||
 OY 1665 ATCGTCTGGAGCGCATG 1682
 |||||
 DB 1178 ILeValLeuGluArgMet 1183
 |||||

RESULT 15

T31093
 probable protein-tyrosine-phosphatase (EC 3.1.3.48) - medicinal leech
 N:Alternate names: receptor tyrosine phosphatase
 C/Species: Hirudo medicinalis (medicinal leech)
 C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
 C/Accession: T31093
 R/Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.
 submitted to the EMBL Data Library, December 1997
 A/Description: Two receptor tyrosine phosphatases expressed by neurons and muscle cells
 A/Reference number: Z20976
 A/Accession: T31093
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1437 <GER>
 A/Cross-references: EMBL:AF017084; NID:G2695656; PIDD:G2695657; PIDD:AB91461.1
 C/Genetics:
 A/Gene: LARI
 C/superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology/
 ogy
 C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

Alignment Scores:

Pred. No.:	4,376-26	Length:	1437
Score:	40.00	Matches:	40

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.51%	Indels:	0
DB:	2	Gaps:	0

US-09-719-272-1 (1-3467) x T31093 (1-1437)

OY 1416 GAGTCAACATGCCCCAGTATATCTGCGTGAATTCAAGTTCACGATGCCCGGATGG 1475
 |||||
 DB 1294 GIuTYrAsnMetProGlnTyrIleLeuArgGluPheLyValThrAspAlaArgAspGly 1313
 |||||
 OY 1476 CAGTCAAGGACAAATCCGAGATTCCAGTTCAAGACTGCGCAGAGCAGGCGTCCCAAG 1535
 |||||
 DB 1314 GlnSerArgThrIleArgGlnPheGlnPheThrArgTrpProGluGlnGlyValProLyS 1333
 |||||

Search completed: March 9, 2004, 09:12:29
 Job time : 106 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 9, 2004, 08:57:13 ; Search time 34 Seconds
(without alignments)

10528.661 Million cell updates/sec

Title: US-09-719-272-1

Sequence: 1138
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Scoring table:

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Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 389414 seqs, 51625971 residues

Word size: 1

Total number of hits satisfying chosen parameters: 663654

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_AA -OPMT=faasan -SUFFIX=rai -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09719272 @CGN 1.1.38 @runat.09032004.085231.7497 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESUBSTRY -NEG_SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database:

Issued_Patents_AA:
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3: /cgm2_6/ptodata/2/iaa/6A.COMB.dep.*
4: /cgm2_6/ptodata/2/iaa/6B.COMB.dep.*
5: /cgm2_6/ptodata/2/iaa/PCTUS.COMB.dep.*
6: /cgm2_6/ptodata/2/iaa/backfile1.dep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	289	25.4	289	1	US-08-036-210-13
2	289	25.4	289	1	US-08-049-609-13
3	289	25.4	289	4	US-09-361-096A-13
4	202	17.8	250	2	US-08-685-992-7
5	202	17.8	250	2	US-09-144-925-7
6	197	17.3	245	2	US-08-685-992-26
7	197	17.3	245	2	US-09-144-925-26
8	95	8.3	245	2	US-08-202-389-21
9	59	5.2	1501	1	US-08-447-464-3
10	59	5.2	1501	1	US-08-716-679-3
11	59	5.2	1911	1	US-08-348-068-5
12	59	5.2	1911	2	US-08-800-825A-5

13	59	5.2	1911	3	US-09-158-657-5	Sequence 5, Appl1
14	59	5.2	1911	5	PCT-US94-10166-5	Sequence 5, Appl1
15	47	4.1	95	1	US-08-202-389-22	Sequence 22, Appl1
16	31	2.7	95	1	US-08-202-389-23	Sequence 23, Appl1
17	14	1.2	14	2	US-08-480-190-241	Sequence 241, App
18	14	1.2	14	2	US-08-488-379-241	Sequence 241, App
19	14	1.2	14	4	US-08-475-399A-241	Sequence 241, App
20	20	1.2	14	5	PCT-US93-07545-241	Sequence 241, App
21	14	1.2	176	1	US-08-036-210-9	Sequence 9, Appl1
22	14	1.2	176	2	US-08-449-609-9	Sequence 9, Appl1
23	14	1.2	176	4	US-09-361-096A-9	Sequence 47, Appl1
24	14	1.2	289	4	US-08-036-210-11	Sequence 11, Appl1
25	14	1.2	322	2	US-08-449-609-11	Sequence 11, Appl1
26	14	1.2	322	2	US-09-361-096A-11	Sequence 11, Appl1
27	14	1.2	322	4	US-09-361-096A-15	Sequence 15, Appl1
28	14	1.2	401	4	US-08-449-609-15	Sequence 15, Appl1
29	14	1.2	402	2	US-08-036-210-15	Sequence 22, Appl1
30	14	1.2	898	1	US-08-036-210-22	Sequence 22, Appl1
31	14	1.2	898	2	US-08-449-609-22	Sequence 22, Appl1
32	14	1.2	898	4	US-09-361-096A-22	Sequence 22, Appl1
33	14	1.2	898	4	US-08-015-985-5	Sequence 5, Appl1
34	12	1.1	235	4	US-09-280-597-5	Sequence 6, Appl1
35	12	1.1	235	4	US-09-280-597-6	Sequence 6, Appl1
36	12	1.1	236	4	US-09-280-597-6	Sequence 7, Appl1
37	12	1.1	242	1	US-09-280-597-7	Sequence 7, Appl1
38	12	1.1	242	4	US-08-015-985-9	Sequence 9, Appl1
39	12	1.1	248	1	US-09-848-294-10	Sequence 10, Appl1
40	12	1.1	248	4	US-09-280-597-9	Sequence 10, Appl1
41	12	1.1	248	4	US-08-685-992-10	Sequence 11, Appl1
42	12	1.1	253	2	US-08-685-992-11	Sequence 11, Appl1
43	12	1.1	253	2	US-09-144-925-10	Sequence 10, Appl1
44	12	1.1	253	2		
45	12	1.1	253	2		

ALIGNMENTS

RESULT 1
US-08-036-210-13
Sequence 13, Application US/08036210
Patent No. 5585233
GENERAL INFORMATION:
APPLICANT: Molier, Niels P.H.
APPLICANT: Molier, Karin B.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
PHOSPHATASE
TITLE OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSES: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 289 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-036-210-13

Alignment Scores:

Pred. No.:	1,536-257	Length:	289
Score:	289.00	Matches:	289
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	25.40%	Indels:	0
DB:	1	Gaps:	0

US-09-719-272-1 (1-3467) x US-08-036-210-13 (1-289)

```

OY 81 ATGGGAGACCAACCCATCCCATCCATCCAGCCTGGGAGCAACATCGAGCGCTCAAA 140
DB 1 MetArgAspHisProProlleProIleThrAspLeuAlaAspAsnIleGluArgLeuLys 20
OY 141 GCCAAGCATGGCTCAAGTTCCTCCAGAGATATGATGCCATGACCCCTGGACAGCATGTC 200
DB 21 AlaAsnAspGlyLeuLysPheSerGlnGluSerIleAspProGlyGlnGlnPhe 40
OY 201 ACGTGGAGATTTCAACCTGGAGGTGAACAAGCCCAAGAACCGCTATGCGAATGTCATC 260
DB 41 ThrTgPgluAsnSerAsnLeuGluValAsnLysProLysAsnArgTyrAlaAsnValIle 60
OY 261 GCCATGACCACTCTCGAGTACTCTTACTTATCGATGGGTCCCGGAGATGATCATC 320
DB 61 AlaTyrAspHisSerIleValIleLeuThrSerIleAspGlyValProGlySerAspTyr 80
OY 321 ATCAATGCCAATCATCATGATGGCTACCGCAGCAGAAATGCTCATGCGCAGCAGGCGC 380
DB 81 IleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGly 100
OY 381 CCCCTGGCCGAGACCATGGGCGCAATTTCTGAGAAATGGTGTGGAAACAGCGCAGCCACT 440
DB 101 ProlLeuProGluThrMetGlyAspPheIlePargMetValTgPgluArgThrAlaThr 120
OY 441 GTGGTCATATGACACAGCGCTGGAGAGAGAGTCCCGGGTAAATGTGATCATGACTGCGCA 500
DB 121 ValValMetMetThrArgLeuGlnGluLysSerArgValLysCysAspGlnTyrTrpPro 140
OY 501 GCCCTGGAGACCGAGACCTGTGGCTTATTCAGGTGACCTGTTGGACACAGTGAAGCTG 560
DB 141 AlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuAspThrValGluLeu 160
OY 561 GCCACATACCTGTGGGACCTTGGACCTCCCAAGAGTGGCTCCGATGAGAGAGGTAG 620
DB 161 AlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySerSerGluLysArgGlu 180
OY 621 CTGGCTGAGTTTCAATTCATGCTGCTGGCCAGACCATGAGATTCTTGATGATCCCACTCC 680
DB 181 LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrProThrPro 200
OY 681 ATCTGGCTTCTCTCAAGACGGGTCAAGGCTGCAACCCCTTAAGCGCAGGCGCCATGGTG 740
DB 201 IleLeuAlaPheLeuAlaArgValLysValaCysAsnProLeuAspAlaGlyProMetVal 220
OY 741 GTGACATGACCGGCGGCTGGGCGGACCGGCTGTTCATCGTGAATGATGCGCATGTG 800
DB 221 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeu 240
OY 801 GAGCGATGAAGACCGAGAGAGCGGTGACATCTATGGCCAGCTGACCTGGACAGCATCA 860
DB 241 GluArgMetLysHisGluLysThrValAspIleTyrIleValIleThrCysMetArgSer 260
OY 861 CAGAGAACTCATGTGTCAGACGAGACAGACCATGATGTTTCATCATGAGGCGCTGCTG 920
DB 261 GlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGluAlaLeuLeu 280

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OY 921 GAGCTGCCAGCTGGCGCCACACAGAG 947
 DB 261 GluAlaAlaThrCysGlyHisThrGlu 289

RESULT 2

US-08-449-609-13

Application US/08449609

Sequence 13 Patent No. 5952212

GENERAL INFORMATION:

APPLICANT: Moller, Niels P.H.

APPLICANT: Moller, Karin B.

TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE

NUMBER OF INVENTIONS: 45

CORRESPONDENCE ADDRESS:

ADDRESSER: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,609

FILING DATE: 24-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/036,210

FILING DATE: 23-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Mierstock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7683-025

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 289 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

Alignment Scores:

Pred. No.:	1,536-257	Length:	289
Score:	289.00	Matches:	289
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	25.40%	Indels:	0
DB:	2	Gaps:	0

US-09-719-272-1 (1-3467) x US-08-449-609-13 (1-289)

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OY 81 ATGGGAGACCAACCCATCCCATCCATCCAGCCTGGGAGCAACATCGAGCGCTCAAA 140
DB 1 MetArgAspHisProProlleProIleThrAspLeuAlaAspAsnIleGluArgLeuLys 20
OY 141 GCCAAGCATGGCTCAAGTTCCTCCAGAGATATGATGCCATGACCCCTGGACAGCATGTC 200
DB 21 AlaAsnAspGlyLeuLysPheSerGlnGluSerIleAspProGlyGlnGlnPhe 40
OY 201 ACGTGGAGATTTCAACCTGGAGGTGAACAAGCCCAAGAACCGCTATGCGAATGTCATC 260
DB 41 ThrTgPgluAsnSerAsnLeuGluValAsnLysProLysAsnArgTyrAlaAsnValIle 60

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QY 261 GCCTAGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 61 AATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
QY 321 ATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 81 AATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
QY 381 CCCCTGCGGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 101 Proleuprogilummetglaaphepmetvaltrpoglulnrglthralatn 120
QY 441 GTGGTCATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 121 ValValmetmetthraagluuglulyserserargValysCyaspglnlrytrp 140
QY 501 GCGGTCGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 141 AATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
QY 561 GCCATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 161 AATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
QY 621 CTGGTCATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 181 LeuarglInpneglInpmetvalatrpProaspheglValProglulnrglthralatn 200
QY 681 ATGCTGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 201 IleuvalapheleuargValysalCyaspglnlrytrpProaspheglValProglulnrglthralatn 220
QY 741 GTGGTCATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 221 ValHiscysseralaglyValargThrglyCyaspglnlrytrpProaspheglValProglulnrglthralatn 240
QY 801 GAGGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 241 GluargmetlyshlslylvalysalCyaspglnlrytrpProaspheglValProglulnrglthralatn 260
QY 861 CAGAGACTATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 261 GluargmetlyshlslylvalysalCyaspglnlrytrpProaspheglValProglulnrglthralatn 280
QY 921 GAGGTCGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 281 GluvalaIatnrcysgllyhlsThrglu 289

```

RESULT 3
 US-09-361-096A-13
 Sequence 13, Application US/09361096A
 Patent No. 6492495
 GENERAL INFORMATION:
 APPLICANT: MOELLER, NIELS P.H.
 APPLICANT: MOELLER, KARIN B.
 APPLICANT: ULRICH, AXEL
 TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
 FILE REFERENCE: 038602/0686
 CURRENT APPLICATION NUMBER: US/09/361,096A
 PRIOR FILING DATE: 1999-07-26
 PRIOR APPLICATION NUMBER: 08/449,609
 PRIOR FILING DATE: 1995-05-24
 PRIOR APPLICATION NUMBER: 08/036,210
 PRIOR FILING DATE: 1995-03-23
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: Patent Ver. 2.1
 SEQ ID NO 13
 LENGTH: 289
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: LAR

US-09-361-096A-13
 Alignment Scores:
 Pred. No.: 1,53e-257 Length: 289
 Score: 289.00 Matches: 289
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 25.40% Indels: 0
 Gaps: 4

US-09-719-272-1 (1-3467) x US-09-361-096A-13 (1-289)

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QY 81 ATGGAAGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 140
DB 1 Metargasphepmetvaltrpoglulnrglthralatn 20
QY 141 GCGGTCGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 200
DB 21 AATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 260
QY 201 AGTGGGAAATTCATGATGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 260
DB 41 ThrtrpgluanserashlslylvalysalCyaspglnlrytrpProaspheglValProglulnrglthralatn 60
QY 261 GCCTAGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 61 AATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 380
QY 321 ATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 81 AATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 380
QY 381 CCCCTGCGGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 101 Proleuprogilummetglaaphepmetvaltrpoglulnrglthralatn 120
QY 441 GTGGTCATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 121 ValValmetmetthraagluuglulyserserargValysCyaspglnlrytrp 140
QY 501 GCGGTCGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 141 AATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 160
QY 561 GCCATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 161 AATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 180
QY 621 CTGGTCATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 181 LeuarglInpneglInpmetvalatrpProaspheglValProglulnrglthralatn 200
QY 681 ATGCTGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 201 IleuvalapheleuargValysalCyaspglnlrytrpProaspheglValProglulnrglthralatn 220
QY 741 GTGGTCATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 221 ValHiscysseralaglyValargThrglyCyaspglnlrytrpProaspheglValProglulnrglthralatn 240
QY 801 GAGGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 241 GluargmetlyshlslylvalysalCyaspglnlrytrpProaspheglValProglulnrglthralatn 260
QY 861 CAGAGACTATGATGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 261 GluargmetlyshlslylvalysalCyaspglnlrytrpProaspheglValProglulnrglthralatn 280
QY 921 GAGGTCGACCACTGAGGATCCTTACTATGATGAGGAGTCCCGGAGTACTAC 320
DB 281 GluvalaIatnrcysgllyhlsThrglu 289

```

RESULT 4

LENGTH: 250 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-144-925-7

Alignment Scores:

Pred. No.:	2,14e-177	Length:	250
Score:	202.00	Matches:	250
Percent Similarity:	97.66%	Conservative:	0
Best Local Similarity:	97.66%	Mismatches:	0
Query Match:	17.75%	Indels:	6
DB:	2	Gaps:	0

US-09-719-272-1 (1-3467) x US-09-144-925-7 (1-250)

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QY 195 CAGTTCACTGGGGAATTCAAACCTGGAGTGAACCAAGCCCAAGCGCTATGGGAAT 254
DB 1 GlnPheThrTrpGluAsnSerAsnLeuGluValAsnProGlyAsnArgYrAlaAsn 20
QY 255 GTCAATGCGCTACAGCACTCTGAGTCATCTTACTCTATGATGGCGTCCCCGGAGAT 314
DB 21 ValIleAlaIleArgPheSerArgValIleIleuThrSerIleAspGlyValProGlySer 40
QY 315 GACTACATCAATGCCAATCATCATGATGCTACCGCAAGCAAGATGCTTACATCGCCAG 374
DB 41 AspTyrIleAsnIleAsnIleAspGlyTyrArgIleGlnIleAsnIleAlaThr 60
QY 375 CAGGGCCCCCGCCGAGACCATGGGAGATTCCTGAGAAATGGTGGGAACAGCCAGC 434
DB 61 GlnGlyProLeuProGlnIleuThrMetGlyAspPheTrpArgMetValIleProGlnIleuThr 80
QY 435 GCCACTGTGTCATGATGACACGCGCTGAGAGAGAAAGTCCCGGTAATGTATCATGATAC 494
DB 81 AlaThrValIleMetMetThrArgLeuGlnIleuIleuSerArgValIleCysAspGlnTyr 100
QY 495 TGGCAGCGCCCTGGCAACCGGACCTGGGCTTATTCAGAGTACCCCTGGTGAACAGCAGT 554
DB 101 TrpProAlaArgGlyThrGlnIleuThrCysGlnIleuIleGlnValIleuLeuAspThrVal 120
QY 555 GAGCTGGCCATCACTGATGCGGACCTTGGCACTCCCAAGAGTGGCTCCAGTGAAG 614
DB 121 GluIleuAlaThrTyrThrVal-----PheAlaIleuHisIleuSerGlySerGlnIleu 138
QY 615 CGTAGCTGCTGCTGCTTCACTTCAATGCTCGGCAAGCAATGAGTTCCTGAGTACCA 674
DB 139 ArgGluLeuArgGlnIleuPheGlnPheMetAlaTrpProAspHisGlyValProGlnTyrPro 158
QY 675 ACTCCCATCTGCGCTTCTCTACGACGAGGTCAGAGGCTTCAACCCCTTGAAGCAGGCGCC 734
DB 159 ThrProIleLeuAlaPheLeuAlaArgValIleValIleCysAsnProLeuAspAlaGlyPro 178
QY 735 ATGTGTGTGTCATGACAGCGCGGCTGGGCGGACCGGCTGCTTCAATCGATGATGATGCC 794
DB 179 MetValIleHisCysSerAlaGlyValIleGlyThrGlyCysPheIleValIleAspAla 198
QY 795 ATGTGTGAGCGGATGAACGACGAGAAAGCGGTGACATCTATGGCCAGTGAACCTGATG 854
DB 199 MetLeuGlnIleuArgMetIleHisGlnIleuThrValAspIleTyrGlnIleHisValThrCysMet 218
QY 855 CGATCAACAGAGAACTTACATGCTGTCAGACGAGAGACCGATACGCTTATTCATCAGAGGCG 914
DB 219 ArgSerGlnIleuArgAsnIleuMetValGlnIleuThrGluAspGlnIleuValPheIleHisGlnIleu 238
QY 915 CTGCTGAGAGGCTGCCACGTCGCGGACCAAGAGGTG 950
DB 239 LeuLeuGlnIleuAlaIleThrCysGlyHisThrGlnIleuVal 250

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RESULT 6
 US-08-685-992-26
 ; Sequence 26, Application US/08685992
 ; Patent No. 5912138

GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas
 APPLICANT: Flint, Andrew J.
 TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 TITLE OF INVENTION: TYROSINE PHOSPHATASES
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESS: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 STREET: Two Millitia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FASTSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/685,992
 FILING DATE: 25-JUL-1996
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCES/DOCKET NUMBER: CSH196-03
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-6240
 TELEFAX: 781-861-9540
 TELEX:

INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 245 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-685-992-26

Alignment Scores:	Pred. No.:	8,64e-173	Length:	245
Score:	197.00	Matches:	245	
Percent Similarity:	97.61%	Conservative:	0	
Best Local Similarity:	97.61%	Mismatches:	0	
Query Match:	17.31%	Indels:	6	
DB:	2	Gaps:	0	

US-09-719-272-1 (1-3467) x US-08-685-992-26 (1-245)

```

QY 1062 ACGTCCCGCTTCATGACGCGCAACCTGCTGCAACAAATTGACACCGGCTGTGTAAC 1121
DB 1 ThrSerArgPheHisSerAlaAsnLeuProCysAsnIleuValIleValIleValIle 20
QY 1122 ATCATGCTTACGAATGACCCGCTGTGTGTCAGAGCCCATCGGAGTGGAGGAGCTCT 1181
DB 21 IleMetProTyrGluLeuThrArgValCysLeuGlnProIleuArgGlyValGlnIleuSer 40
QY 1182 GACTACATCAATGCCAGCTTCTGATGATGTATGACACGACAGAGGCTTACATGACTACA 1241
DB 41 AspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnIleuValIleAlaThr 60
QY 1242 CAGGGGCTCTTGGCAAGAGACCGAGACCTTGGCGGACGCTTANGGAGCAATGCC 1301
DB 61 GlnGlyProLeuAlaIleuSerThrGluAspPheTrpArgMetLeuTrpIleHisAsnSer 80
QY 1302 ACCATCATGTCATGCTGACCAAGCTTCGGAGATGGGAGATGGGAGAAATGCCACAGTAC 1361
DB 81 ThrIleIleValMetLeuThrIleuArgGlnIleuMetGlyArgGlnIleuSerHisGlnTyr 100
QY 1362 TGGCCAGCAGAGGCGCTCTGCTGCTTACCAAGTACTTGTGTGACCCAGATGCGTGAATAC 1421

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Db 101 TTPPQALLAGLWISerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyr 120
 QY 1422 AACATGCCCGCACTATATCTCGTAGTTCAGAGTCACGATGCCCGGATGGGAGTCA 1481
 Db 121 AsnMetProGlnTyrIleLeu-----PheLysValIleThrAspAlaArgAspGlyGlnSer 138
 QY 1482 AGGACAAATCCGGCAGTTCAGTTCACAGACTGGCCAGAGCAGGGCGTCCCAAGACAGC 1541
 Db 139 ArgThrIleArgGlnPheGlnPheThrAspIleProGlnGlnGlnValProLysThrGly 158
 QY 1542 GAGGATTCATTGACTTCATCGGGAGGTGATTAAGACCAAGACGATTGGACAGAT 1601
 Db 159 GluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGluGlnPheGlyGlnAsp 178
 QY 1602 GGGCCATACAGGTGACAGTGTGCTGGCGGGCCGACCGGGGGTTCATCATCTCTG 1661
 Db 179 GlyProIleThrValHisCysSerAlaGlyValGlyAspThrGlyValPheIleThrLeu 198
 QY 1662 AGCATGCTCTGGAGCGCATGCGCTATGAGGGCGTGTGACATGTTTCAACCGTGAAG 1721
 Db 199 SerIleValLeuGlnArgMetArgTyrGlnGlyValValAspMetPheGlnThrValLys 218
 QY 1722 ACCCTGCTACAGAGGTCTCTGCACTGATGTCAGACAGACAGACAGATCAGCTGTAC 1781
 Db 219 ThrLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyrGlnLeuGlyTyr 238
 QY 1782 CGTGGCGCTCGAGTACCTC 1802
 Db 239 ArgAlaAlaLeuGluTyrLeu 245
 RESULT 7
 US-09-144-925-26
 ; Sequence 26, Application US/09144925
 ; Patent No. 5951979
 ; GENERAL INFORMATION:
 ; APPLICANT: Tonks, Nicholas
 ; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 ; TITLE OF INVENTION: TYROSINE PHOSPHATASES
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P. C.
 ; STREET: Two Milcila Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02421-4799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FASTSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,925
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/685,992
 ; FILING DATE: July 25, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: CSHL96-032
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 781-861-6240
 ; TELEFAX: 781-861-9540
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 245 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single

; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-09-144-925-26
 Alignment Scores:
 Pred. No.: 8,64e-173
 Score: 197.00
 Percent Similarity: 97.61%
 Best Local Similarity: 97.61%
 Query Match: 17.31%
 DB: 2
 Gaps: 0
 US-09-719-272-1 (1-3467) x US-09-144-925-26 (1-245)
 QY 1062 ACCGTCCGCTTCATCAAGCCCAAGCTGCTCCCTGCAACAGTTCAAGAACCGGTGTGAAC 1121
 Db 1 ThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsn 20
 QY 1122 ATCATGCCCTAAGAAATTGACCCGCTGTGTCTGTCAGACCCCATCCGTGTGTGAGGGCTCT 1181
 Db 21 IleMetProTyrGlnLeuThrArgValCysLeuGlnProIleArgGlyValGluGlySer 40
 QY 1182 GACTACATCAATGCCAGCTTCTGTGATGTTATAGACAGCAAGAGCTTACATAGCTACA 1241
 Db 41 AspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnLysAlaTyrIleAlaThr 60
 QY 1242 CAGGGCGCTCTGGCAGAGGACACCGAGACTTGTGGCGATGCTATGGAGAGCAATTC 1301
 Db 61 GlnGlyProLeuAlaGlnSerThrGlnAspPheThrArgMetLeuTrpGlnHisAsnSer 80
 QY 1302 ACCATCATGTCATGTCGACCAAGCTTGGAGATGGGAGGAGAAATGCCACCACTAC 1361
 Db 81 ThrIleIleValMetLeuThrLysLeuArgGlnMetGlyArgGlnLysCysHisGlnTyr 100
 QY 1362 TGGCCAGACAGAGGCTTGTGCTGCTCAACAGTACTTGTGTGACCCGATGAGCTGATAC 1421
 Db 101 TTPProAlaGlnArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyr 120
 QY 1422 AACATGCCCGCACTATATCTCGTAGTTCAGATGTCACGATGCCCGGATGGGAGTCA 1481
 Db 121 AsnMetProGlnTyrIleLeu-----PheLysValIleThrAspAlaArgAspGlyGlnSer 138
 QY 1482 AGGACAAATCCGGCAGTTCAGTTCACAGACTGGCCAGAGCAGGGCGTCCCAAGACAGC 1541
 Db 139 ArgThrIleArgGlnPheGlnPheThrAspIleProGlnGlnGlnValProLysThrGly 158
 QY 1542 GAGGATTCATTGACTTCATCGGGAGGTGATTAAGACCAAGACGATTGGACAGAT 1601
 Db 159 GluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGluGlnPheGlyGlnAsp 178
 QY 1602 GGGCCATACAGGTGACAGTGTGCTGGCGGGCCGACCGGGGGTTCATCATCTCTG 1661
 Db 179 GlyProIleThrValHisCysSerAlaGlyValGlyAspThrGlyValPheIleThrLeu 198
 QY 1662 AGCATGCTCTGGAGCGCATGCGCTATGAGGGCGTGTGACATGTTTCAACCGTGAAG 1721
 Db 199 SerIleValLeuGlnArgMetArgTyrGlnGlyValValAspMetPheGlnThrValLys 218
 QY 1722 ACCCTGCTACAGAGGTCTCTGCACTGATGTCAGACAGACAGACAGATCAGCTGTAC 1781
 Db 219 ThrLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyrGlnLeuGlyTyr 238
 QY 1782 CGTGGCGCTCGAGTACCTC 1802
 Db 239 ArgAlaAlaLeuGluTyrLeu 245
 RESULT 8
 US-08-202-389-21
 ; Sequence 21, Application US/08202389
 ; Patent No. 5536636
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman Jr., Robert M.
 ; APPLICANT: Plutsky, Jorge

```

Db      81 GlnPheClyGlnAlaPglYProIleHrValHIScysSerAlaGly 95

RESULT 9
US-08-447-464-3
; Sequence 3, Application US/08447464
; Patent No. 5840842
GENERAL INFORMATION:
APPLICANT: Schlensing, Joseph
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: PHOSPHOTRANSFERASE-SIGMA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,464
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/130,570
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8664/3741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1501 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-447-464-3

Alignment Scores:
Pred. No.:      8.56e-46      Length:      1501
Score:          59.00        Matches:      59
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches:  0
Query Match:      5.18%      Indels:      0
DB:                2          Gaps:            0

US-09-719-272-1 (1-3467) x US-08-447-464-3 (1-1501)
QY      1311 GTCATGCTGACCAAGCTTCGGAGATGCGAGGAGAAATGCCACAGTACTGGCCAGCA 1370
      |||||
Db      1330 VALMELLEUTHRLYLLEuArgLInMetGlyArgGluuysCySHISgIntYTrpProAla 1349
QY      1371 GAGGCGCTGCTGCTGCTACCAAGTACTTTGTGTGACCCGAGGCGTGAGTAAACAATGCC 1430
      |||||
Db      1350 GUAAGSERRALAAArgTYGIntYrHeValValaAPrometAlaIGIntYrAsmMetPro 1365
QY      1431 CAGTAAATCCTCGAGTCAAGTCAAGGTCAAGATGCCCGGAGATGGGCACTCAAGACA 1487
      |||||
Db      1370 GIntYrIleuArgGlnPheLysValIthrSerAlaArgaPglYgInSerArgThr 1388
RESULT 10
US-08-716-679-3
; Sequence 3, Application US/08716679
; Patent No. 5846800

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STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,825A
FILING DATE: 14-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-825A-5

Alignment Scores:
Pred. No.: 8,27e-46 Length: 1911
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
Gaps: 0

US-09-719-272-1 (1-3467) x US-08-800-825A-5 (1-1911)

QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGGAGGAGAAATGCCACCACTACTGCGCCAGCA 1370
DB 1740 ValMetLeuThrIlySleuAArgGluMetGlyArgGluIlyScyShsgIntyYrTPrCoAla 1759
QY 1371 GAGGCGCTGCTGCTGCTACCACTACTTGTGTGACCCGATGGCTGAGTCAACATGCC 1430
DB 1760 GluArgSerAlaArgYrGIntyRheValValAspProMetAlaGIntyRAspMetPro 1779
QY 1431 CAGTATATCTGCTGCTGATTCAGGTCAAGATGCCGATGGGATGGGCACTCAAGACA 1487
DB 1780 GIntyRtleuAArgGluPheIyValThrAspAlaArgAspGlyGlnSerArgThr 1798

RESULT 13
US-09-158-657-5
Sequence 5, Application US/09158657
Patent No. 6214564
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,657
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/800,825
FILING DATE: 14-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-158-657-5

Alignment Scores:
Pred. No.: 8,27e-46 Length: 1911
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
Gaps: 3

US-09-719-272-1 (1-3467) x US-09-158-657-5 (1-1911)

QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGGAGGAGAAATGCCACCACTACTGCGCCAGCA 1370
DB 1740 ValMetLeuThrIlySleuAArgGluMetGlyArgGluIlyScyShsgIntyYrTPrCoAla 1759
QY 1371 GAGGCGCTGCTGCTGCTACCACTACTTGTGTGACCCGATGGCTGAGTCAACATGCC 1430
DB 1760 GluArgSerAlaArgYrGIntyRheValValAspProMetAlaGIntyRAspMetPro 1779
QY 1431 CAGTATATCTGCTGCTGATTCAGGTCAAGATGCCGATGGGATGGGCACTCAAGACA 1487
DB 1780 GIntyRtleuAArgGluPheIyValThrAspAlaArgAspGlyGlnSerArgThr 1798

RESULT 14
PCT-US94-10166-5
Sequence 5, Application PC/TUS9410166
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN III
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10166
FILING DATE: 09-SEPT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032

FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN, JOHN W III
REGISTRATION NUMBER: 35403
REFERENCE/DOCKET NUMBER: 16992
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-10166-5

Alignment Scores:
Pred. No.: 8,27e-46 Length: 1911
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 5 Gaps: 0

US-09-719-272-1 (1-3467) x PCT-US94-10166-5 (1-1911)

QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGGAGAGAAATCCACCACTACTGCGCAGCA 1370
DB 1740 ValMetLeuThrIleuLeuArgGluMetGlyArgGluysCysHsGlnIlyrTTPProAla 1759
QY 1371 GAGCGCTGTGCTGCTACCACTTGTGTGAACCGATGCTGTGATCAACATGCC 1430
DB 1760 GluArgSerAlaArgTyrGlnIlyrPheValValAspPrometAlaGluTyrAsmMetPro 1779
QY 1431 CAGTATCCCTGCGGAGTTCAGGTCAAGATGCCGCGGATGGGAGGTCAAGGACA 1487
DB 1780 GlnIlyrIleuArgGluPheIyValThrAspAlaArgAspGlyGlnSerArgThr 1798

RESULT 15
US-08-202-389-22

Sequence 22, Application US/08202389

Patent No. 5536636

GENERAL INFORMATION:

APPLICANT: Freeman Jr., Robert M.

APPLICANT: Plutsky, Jorge

APPLICANT: Neel, Benjamin G.

APPLICANT: Rosenberg, Robert D.

TITLE OF INVENTION: IDENTIFICATION OF NOVEL TYROSINE

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS: 54

ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Mallitia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/202,389

FILING DATE: 28-FEB-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/983,926

FILING DATE: 01-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/829,141

FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/721,112
FILING DATE: 26-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: B192-05WA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-202-389-22

Alignment Scores:
Pred. No.: 1.45e-34 Length: 95
Score: 47.00 Matches: 47
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.13% Indels: 0
DB: 1 Gaps: 0

US-09-719-272-1 (1-3467) x US-08-202-389-22 (1-95)

QY 1347 AATGGCAACCACTACTGCGCAGCAGAGCGCTGCTGCTACCACTTGTGTGAC 1406
DB 1 LysCysHsGlnIlyrTTPProAlaGluArgSerAlaArgTyrGlnIlyrPheValValAsp 20
QY 1407 CCGATGCTGAGTACCAACATGCCCGATATCTGCTGAGTTCAGGTCAAGATGCC 1466
DB 21 PrometAlaGluTyrAsmMetProGlnIlyrIleuArgGluPheIyValThrAspAla 40
QY 1467 CCGGATGGGCACTCAAGGACA 1487
DB 41 ArgAspGlyGlnSerArgThr 47

Search completed: March 9, 2004, 09:13:29
Job time: 64 secs